

STIC-Biotech/ChemLib

67938

From: Bunner, Bridget  
Sent: Tuesday, June 04, 2002 8:47 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like the following sequence searched for case 09/655,272:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647  
CMI-10D12  
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mailroom 10C01

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

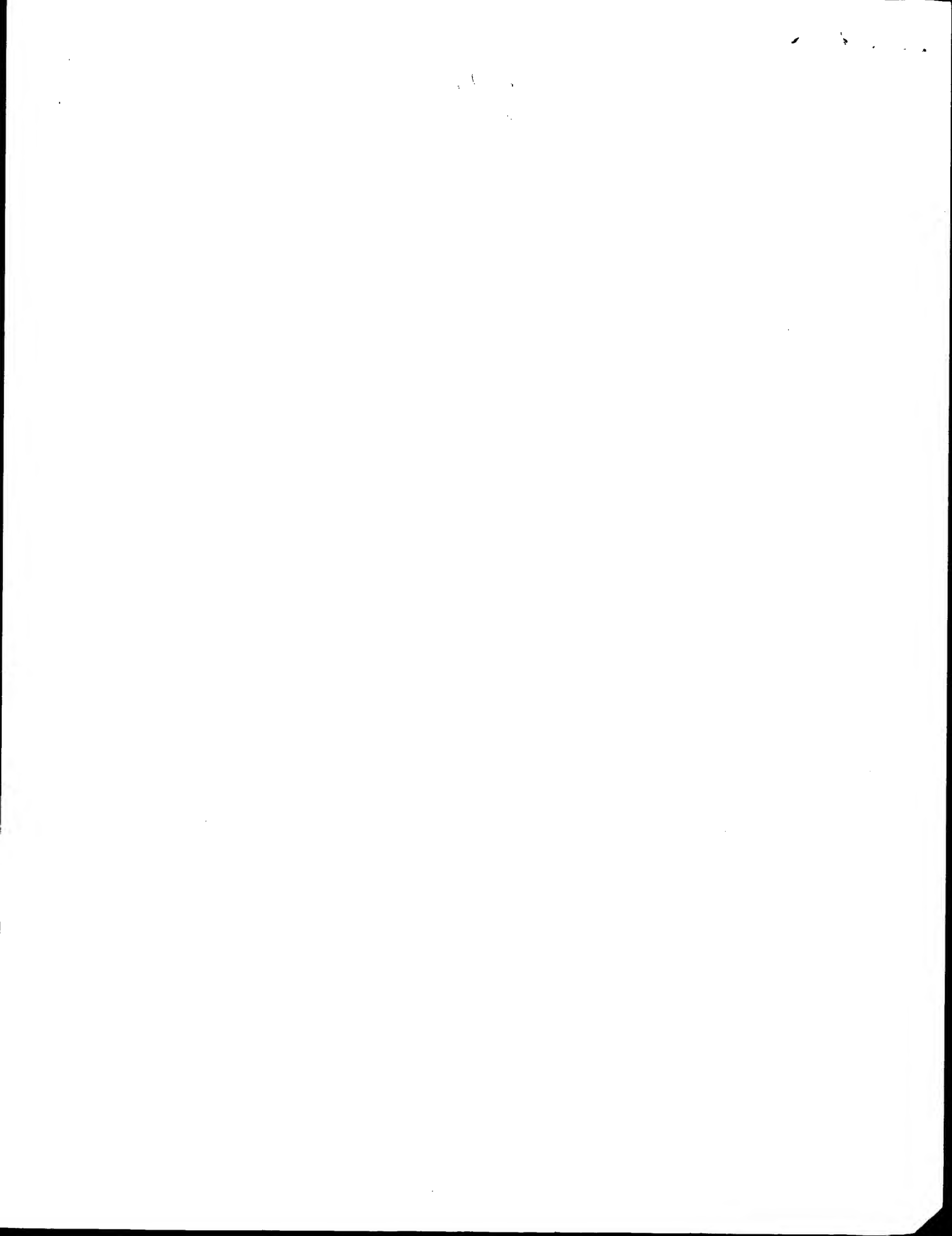
Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 6/4/02  
Date Completed: 6/4/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 1 \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 02 \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 4.5  
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OM protein - protein search, using SW model

```

Run on:      June 4, 2002, 11:00:16 ; Search time 13.41 Seconds
              (without alignments)
              1149.171 Million cell updates/sec

```

Title: US-09-655-272-2  
Perfect score: 2079  
Sequence: 1 MRSTYLLALALVLLVSG.....SKPSPRPGPGRLDKAVPV 398

Scoring table:

BLOSUM62	
Gapop 10.0 , Gapext 0.5	
105224 seqs, 38719550 residues	

Searched: 105224

```

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2079	100.0	398	1	C1W4_MOUSE	088454 homo musculus
2	1692.5	81.4	393	1	C1W4_HUMAN	Q9N968 homo sapien
3	780	38.0	538	1	C1W4_HUMAN	B57789 homo sapien
4	788	37.9	538	1	C1W4_RAT	Q9J134 mus musculus
5	770.5	37.1	411	1	C1W2_MOUSE	P97438 mus musculus
6	759.5	36.5	426	1	C1W2_HUMAN	Q95069 homo sapien
7	416	20.0	439	1	C1W6_HUMAN	Q95279 homo sapien
8	386	18.6	333	1	C1W1_HUMAN	Q92457 homo sapien
9	379.5	18.3	336	1	C1W1_MOUSE	Q00180 homo sapien
10	369.5	17.8	1001	1	ORK1_DROME	Q08581 mus musculus
11	353	17.0	365	1	C1W9_CAVPO	Q94526 drosophila
12	333.5	16.0	409	1	C1W3_MOUSE	Q9J158 cavia porce
13	332.5	16.0	409	1	C1W3_RAT	Q9J111 mus musculus
14	332.5	16.0	411	1	C1W3_HUMAN	Q54112 rattus norv
15	327.5	15.8	374	1	C1W3_HUMAN	Q9N9C2 homo sapien
16	325.5	15.7	394	1	C1W8_MOUSE	Q14649 homo sapien
17	282.5	13.6	307	1	C1W7_HUMAN	Q9azt1 mus musculus
18	260	12.5	335	1	TKR8_CAEEL	Q9yuz2 homo sapien
19	216.5	10.4	691	1	TKR1_YEAST	P44310 caenorhabd
20	168.5	8.1	691	1	SYN1_HUMAN	P34010 saccharomyc
21	132	6.3	705	1	SYN1_HUMAN	P16760 homo sapien
22	131	6.3	1461	1	IE18_PROF	P16765 pseudorabie
23	130	6.3	415	1	SYN1_CANF	Q62732 cantis famill
24	129	6.3	1446	1	IE18_PROF	P33479 pseudorabie
25	125	6.0	704	1	SYN1_RAT	P09951 rattus norv
26	124	6.0	670	1	SYN1_MOUSE	Q88933 mus musculus
27	123.5	5.9	695	1	C1Q4_HUMAN	P56696 homo sapien
28	121	5.8	706	1	SYN1_BOVIN	P17599 bos taurus
29	120.5	5.8	872	1	C1Q2_HUMAN	O43526 homo sapien
30	118	5.7	1159	1	HERG_HUMAN	Q12809 homo sapien
31	115.5	5.6	555	1	GPI_CHICK	Q9F6P6 chlamydomo
32	114.5	5.5	857	1	NFM_CHICK	P16053 gallus gal
33	114	5.5	590	1	PHO4_NECRC	P15710 neurospora

088943	rattus norv	1	852	5.5	113.5	34
001338	mus musculus	1	450	5.4	113	35
09N254	homo sapien	1	2564	5.4	113	36
092351	homo sapien	1	676	5.4	111.5	37
092351	mus musculus	1	759	5.4	111.5	38
P20186	streptomyce	1	348	5.3	111	39
Q13444	homo sapien	1	814	5.3	110	40
P74745	synecdochyst	1	555	5.2	108.5	41
060011	ictalurid h	1	302	5.2	108	42
Q9Xb57	staphylococc	1	358	5.2	108	43
P40603	brassica nap	1	449	5.2	107.5	44
Q03391	mus musculu	1	1323	5.2	107.5	45

## ALIGNMENTS

ID	C1M4-MOUSE	STANDARD:	PRT:	398 AA.
CC	088454:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Potassium channel subfamily K member 4 (TRK-related arachidonic acid-stimulated potassium channel protein) (TRAK).			
CC	KCNK4 GN TRAK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98292450; PubMed=9628867;			
RA	Fluk M., Lesage F., Duprat F., Heutaux C., Reyes R., Fosset M., Lazdunski M.;			
RT	"A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids."			
RL	EMBO J. 17:3297-3308(1998).			
RP	ACTIVATION.			
RA	MEDLINE=99254548; PubMed=10321245;			
RX	Patel A.J., Honore E., Lesage F., Fluk M., Romey G., Lazdunski M.;			
RT	"Inhalational anesthetics activate two-pore-domain background K+ channels."			
RL	Nat. Neurosci. 2:422-426(1999).			
CC	-1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH EXTERNAL K+ CONCENTRATIONS.			
CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).			
CC	-1- SUPRACELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/TRANSLATION/TRANSCRIPT: ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND TESTIS.			
CC	-1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.			
CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
CC	-----			
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CC	EMBL: AF056492; AAC40181.1; .			
DR	MGI: 1298234; Kcnk4.			

		0, mismatches	0, indels	0, gaps
0y	1 MRSSTLLALLALVLLLYLVSGALVFQALEPQEPHEQAOAKKMHGDDQFLRDHPVCYSQKSLSD			
Db	1 MRSSTLLALLALVLLLYLVSGALVFQALEPQEPHEQAOAKKMHGDDQFLRDHPVCYSQKSLSD			
0y	61 FIKLLVHALGGANPETSWTSSNSSHSSANMLGSAFFESGTLITTTIGYGNIYVHTAGRLF			
Db	61 FIKLLVHALGGANPETSWTSSNSSHSSANMLGSAFFESGTLITTTIGYGNIYVHTAGRLF			
0y	121 CIFALVIGIDLPFQMLLAGVDRLGSSLRGIGHIEAIFLKMHWBPGLVRSLSAVLFLDIG			
Db	121 CIFALVIGIDLPFQMLLAGVDRLGSSLRGIGHIEAIFLKMHWBPGLVRSLSAVLFLDIG			
0y	181 CLIFLVLTPTFEVSVMESMKLEAIFYVYLTITVWGFQDYVDGDTGQNSPAVQGLVWFMT			
Db	181 CLIFLVLTPTFEVSVMESMKLEAIFYVYLTITVWGFQDYVDGDTGQNSPAVQGLVWFMT			
0y	241 LFGLVAFVSVLTITGNMLRAVSRRTRAEMGSLTFOAASWTCVTYARVYORTGCSAPPEK			
Db	241 LFGLVAFVSVLTITGNMLRAVSRRTRAEMGSLTFOAASWTCVTYARVYORTGCSAPPEK			
0y	301 EOPLLPSSLPPAPVVEBAGRPSPAAEKEVETPSPATASALDYPSENLAFLIDESDTS			
Db	301 EOPLLPSSLPPAPVVEBAGRPSPAAEKEVETPSPATASALDYPSENLAFLIDESDTS			
0y	361 ERGALTRAPBGRRRRPNPSKPSRPGRPGTLRHXAPV			
Db	361 ERGALTRAPBGRRRRPNPSKPSRPGRPGTLRHXAPV			

RESULT	ID	STANDARD	PRT	393 AA.
2	CIW4_HUMAN			
AC	Q9NYG8			
DT	16-OCT-2001 (rel. 40, Created)			
DT	16-OCT-2001 (rel. 40, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Potassium channel subfamily K member 4 (TWIK-related stimulated potassium channel protein) (TRAAK).			
DE	KCNK4 OR TRAAK.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
PN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			

RX MEDLINE=20499203; PubMed=11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A.,  
 RA Kelsell J.E., Murdoch P.R., Randall A.D., Rennie G.I., Gloger I.S.,  
 RT "Cloning, localisation and functional expression of a novel human,  
 RT cerebellum specific, two pore domain potassium channel.",  
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RP [2].  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Frontal cortex;  
 RA Gray A.T.;  
 RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to  
 RT chromosome 11";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20231699; PubMed=10767409;  
 RA Lesage F., Maignret F., Ladzinski M.;  
 RT "Cloning and expression of human TRAAK, a polyunsaturated fatty  
 RT acids-activated and mechano-sensitive K(+) channel.";  
 RL FASEB Lett. 471:137-140(2000).  
 RC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH  
 CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
 CC CHANNELS BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM

CC	-----	
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CC	or send an email to <a href="mailto:license@isb-slb.ch">license@isb-slb.ch</a> ).	
DR	-----	
DR	EMBL; AF248242; AAC31731.1; AL-	
DR	EMBL; AF247042; AAF64062.1; ALT_INIT.	
DR	MIM; 605720;	
DR	InterPro; IPR003280; 2PoreK_channel.	
DR	InterPro; IPR00636; CatIon_chan_non_1lg.	
DR	InterPro; IPR001622; Channel_pore_K.	
DR	Pfam; PF00520; Ion_trans_1.	
DR	Pfam; PF02168; Occludin_1.	
KW	PRINTS; PR01333; 2POREKANAL.	
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport;	
FT	Glycoprotein.	
FT	DOMAIN	1
FT	TRANSMEM	3
FT	DOMAIN	4
FT	TRANSMEM	89
FT	DOMAIN	113
FT	TRANSMEM	118
FT	DOMAIN	138
FT	TRANSMEM	140
FT	TRANSMEM	171
FT	TRANSMEM	172
FT	TRANSMEM	192
FT	TRANSMEM	221
FT	DOMAIN	234
FT	TRANSMEM	254
FT	DOMAIN	255
FT	CARBOHYD	78
FT	CARBOHYD	78
FT	CARBOHYD	82
FT	CARBOHYD	82
FT	CONFLICT	328
FT	CONFLICT	328
SEQUENCE	393 AA; 42704 MW; 7F1B53A0A9AD57D CRC64;	

Query Match	81.4%	Score 1692.5	DB 1	Length 393
Best Local Similarity	82.4%	Pred. No. 1.9e-84		
Matches	329	Conservative	24	Mismatches 41
				Indels 5
				Gaps 2
QY	1	MRSTLLALLALVLLVLYSGALVFOALEPQPHQOAKMDGSRQFLRDHPVCYSOKSLSD	60	
Db	1	MRSTLLALLALVLLVLYSGALVFOALEPQPHQOAKMDGSRQFLRDHPVCYSOKSLSD	60	
	61	FILLVLEALGGANPESTWTSNNSHSSAMNIGSAFPSSGILITTTIGGYNIVLHTTAGRGF	120	
QY	:			
	:			



```

QY      1 MRSTLLALLLVLLVYSGALVFQALEDPHEEQQAOKKMHGRDQFLRDHPVCSQKSLD 60
      | : : : | : | : | : | : | : : : : : : | : | : | : | : | :

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Db 42 MKKTVSTFLVVLVLLIGAAVEKALEOPQISQRTIVIOKQFIAGHACVNSTELDE 101
QY 61 FIKLVEALGGANPETSWTSSNNHSSAMNLSAEPFGSTITITIGNIVLHTDAGRLE 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 102 LIQOIVAAIMAGIIP---LGNSNQVSHWDLGSSFFFACTVITITIGFINSRTEGKIF 158
QY 121 CIFVALVGIPLFEGMLLAGVDRGLSSLRGIGIEAIFLKMHPGGLVRSLSAVFLILIG 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 159 CIIVALLGIPLFEGFLLAGVDQGLTIFGKIAKVEDTPIKMNVSQTKIRIISTIFILFG 218
QY 181 CLLEFLVLPFVFVSYSMSKLEAIFVIVLTITVFGDYPDGTGQNSPAYOPLVFWMI 240
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 219 CVLFAVLPVAFIEFKHIEGWSALDAIFVIVLTITVFGDYPVAGSDIEYDFFKPVVFWMI 278
QY 241 LFLGLAFASVLTITIGNMLRAVSRRTAEKGGTLQAASWTGVTYA 285
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 279 LVGLAFPAVLISMIGMLRVISKRTEVEGFRRAHAEMTANYTA 323

RESULT 6
C1W2_HUMAN STANDARD: PRT: 426 AA.
AC 095069: Q9UNE3: 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
DE channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
DE potassium channel TRK1).
GN KONK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99354548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RT Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price E.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RT Submitted (May-1997) to the EMBL/Genbank/DBSJ databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC CHLOROFORM, HALOTHANE AND ISOFURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
CC EMBL: AF129399; AAD47569.1; -
CC EMBL: AF004711; AAD01203.1; -
CC MIM: 603219; -
CC InterPro: IPR003280; 2porek_channel.
CC InterPro: IPR000636; Cation_chan_non_lig.
CC InterPro: IPR001622; Channel_pore_K.
CC InterPro: IPR003976; Trek_channel.
CC Pfam: PF00520; Ion_trans_1.
CC PRINTS: PR01333; 2PORECHANNEL.
CC PRINTS: PR01499; TREKCHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Potassium transport;

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KM Glycoprotein. 1 61
FT DOMAIN 1 61
FT TRANSMEM 62 82
FT TRANSMEM 144 170
FT TRANSMEM 172 192
FT TRANSMEM 193 223
FT TRANSMEM 224 244
FT TRANSMEM 253 283
FT TRANSMEM 288 308
FT DOMAIN 309 426
FT DOMAIN 378 426
FT DOMAIN 354 426
FT CARBOHYD 110 110
FT CARBOHYD 134 134
FT CONFLICT 2 16
FT CONFLICT 309 311
FT CONFLICT 391 391
FT CONFLICT 411 411
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009FAE CRC64;

Query Match 36.5%; Score 759.5; DB 1; Length 426;
Best Local Similarity 49.1%; Pred. No. 2.2e-34;
Matches 140; Conservative 57; Mismatches 85; Indels 3; Gaps 1;

QY 1 MRSTLLALLALVLYVSGALVFOALEPHEQQAOKMDHGRQFLRDHCVCQSKSLSD 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 57 MKKTVSTFLVVLVLLIGAAVEKALEOPQISQRTIVIOKQFIAGHACVNSTELDE 116
QY 61 FIKLVEALGGANPETSWTSSNNHSSAMNLSAEPFGSTITITIGNIVLHTDAGRLE 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 117 LIQOIVAAIMAGIIP---LGNSNQVSHWDLGSSFFFACTVITITIGFINSRTEGKIF 173
QY 121 CIFVALVGIPLFEGMLLAGVDRGLSSLRGIGIEAIFLKMHPGGLVRSLSAVFLILIG 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 174 CIIVALLGIPLFEGFLLAGVDQGLTIFGKIAKVEDTPIKMNVSQTKIRIISTIFILFG 233
QY 181 CLLEFLVLPFVFVSYSMSKLEAIFVIVLTITVFGDYPDGTGQNSPAYOPLVFWMI 240
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 234 CVLFAVLPVAFIEFKHIEGWSALDAIFVIVLTITVFGDYPVAGSDIEYDFFKPVVFWMI 293
QY 241 LFLGLAFASVLTITIGNMLRAVSRRTAEKGGTLQAASWTGVTYA 285
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 294 LVGLAFPAVLISMIGMLRVISKRTEVEGFRRAHAEMTANYTA 338

RESULT 7
C1W5_HUMAN STANDARD: PRT: 499 AA.
AC 095279: 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 5 (Acid-sensitive potassium
DE channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
GN KONK5 OR TASK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99030343; PubMed=9812978;
RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
RA Lazdunski M.;
RT "Cloning and expression of a novel pH-sensitive two pore domain K+
RT channel from human kidney.";
RT J. Biol. Chem. 273:30863-30869(1998).
CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL

```





DR EMBL: AF281302; AAG10506.1; -  
 DR DR MIM: 603939; -  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR InterPro: IPR001622; Channel\_pore\_K.  
 DR InterPro: IPR001779; TWIK1\_channel.  
 DR Pfam: PF00520; Ion\_trans. 1.  
 DR PRINTS: PR01096; TWIK1CHANNEL.  
 DR Ionic channel: Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein; Alternative splicing  
 FT DOMAIN 1 4  
 FT TRANSMEM 5 25  
 FT DOMAIN 90 115  
 FT TRANSMEM 121 141  
 FT DOMAIN 142 172  
 FT TRANSMEM 173 193  
 FT DOMAIN 199 223  
 FT TRANSMEM 236 256  
 FT DOMAIN 257 313  
 FT CARBOHYD 79 79  
 FT CARBOHYD 85 85  
 FT VARSPIC 1 134  
 FT MOTAGEN 53 53  
 SQ SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;

Query Match 18.6%; Score 386; DB 1; Length 313;  
 Best Local Similarity 34.8%; Pred. No. 1.8e-14;  
 Matches 111; Conservative 51; Mismatches 131; Indels 26; Gaps 10;

QY 1 MRSTLLA-LTALVLYSGALVQALPEQHEQAKMDHGRDQFLRHPVCSQSKLE 59  
 DB 1 MRGALLAGLAAVAAALVGLALVRLGEPHRLRALETLRAQLQSPCAAPALD 60  
 QY 60 DFILVLEALGCGANPEFTSMNSNHS-AMNLSAFEFSGTITITIGYCNIVLHTDAGR 118  
 DB 61 AFVERVLAAGLGRVYLANSGSNASDPAMDFAALFPSTLITTYGYTPPLTDAGK 120  
 QY 119 LFCIFYALVIGLPGMLAGVDRGLSSLRGIGHIEALF--KWHVPGLVRSLSAVLF 176  
 DB 121 AFSLAFALGVPTTLLLTASQRLSLTLT---HVLPSLWSLWGMGMDPR--RAACWHLV 174  
 QY 177 LLIGCLLV--LTPEFVSVM-ESMSKLEATYFIVLTITVGFQDYGQDGTGNSPA-Y 232  
 DB 175 ALIGVAVVCELVPAVIFAHLEAMSFDAVYFCFISTIGLGDYVGEARQPYRALY 234  
 QY 233 QPLVFWILFGLAFASVLTITGNMLRAVSRRTAEMGLF--AQAASWTGTVTARYTQ 289  
 DB 235 KVLVYVLEFLGVAMVLYLQTF-----RHVSDHLGTELILLPPCPASFNADDD 285  
 QY 290 RTGPSAPPEKEQPLPSS 308  
 DB 286 RVDILGPOPESHQOLSSASS 304

RESULT 9  
 C1WL\_HUMAN STANDARD; PRT; 336 AA.  
 AC 000180; Q13307;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily k member 1 (Inward rectifying potassium  
 channel protein TWIK-1) (Potassium channel KCNK1).  
 GN KCNK1 OR TWIK1 OR HOH1 OR KCNK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.  
 RC TISSUE-Kidney;  
 RX MEDLINE=96183184; PubMed=8605869;

RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,  
 RA Barhanin J.,  
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K<sup>+</sup> channel with a  
 RT novel structure."  
 RL EMBO J. 15:1004-1011(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND REVIEW.  
 RC TISSUE-Brain;  
 RX MEDLINE=96122696; PubMed=9462864;  
 RA Goldstein S.A.N., Wang K.-W., Ilian N., Pausch M.H.;  
 RT "Sequence and function of the two P domain potassium channels:  
 RT implications of an emerging superfamily."  
 RL J. Mol. Med. 76:13-20(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96026667; PubMed=9362344;  
 RA Orlas M., Velazquez H., Tung F., Lee G., Desir G.V.;  
 RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive  
 RT expression in distal nephron segments."  
 RL Am. J. Physiol. 273:F663-F666(1997).  
 CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND  
 CC BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.  
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND  
 CC INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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 CC -----  
 DR EMBL: U33632; AAB01688.1; -  
 DR EMBL: U76996; AAB97878.1; -  
 DR EMBL: U90065; AAB51147.1; -  
 DR MIM: 601745; -  
 DR InterPro: IPR003280; 2poreK\_channel.  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR InterPro: IPR001622; Channel\_pore\_K.  
 DR InterPro: IPR001779; TWIK1\_channel.  
 DR Pfam: PF00520; Ion\_trans. 1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 DR PRINTS: PR01096; TWIK1CHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 20  
 FT TRANSMEM 21 41  
 FT DOMAIN 104 130  
 FT TRANSMEM 133 153  
 FT DOMAIN 154 177  
 FT TRANSMEM 178 198  
 FT DOMAIN 212 238  
 FT TRANSMEM 247 267  
 FT DOMAIN 268 336  
 FT CARBOHYD 95 95  
 FT MOTAGEN 161 161  
 SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

Query Match 18.3%; Score 379.5; DB 1; Length 336;  
 Best Local Similarity 34.4%; Pred. No. 4.2e-14;  
 Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

QY 2 RSTLLALLA-LVLYVSGALVQALPEQHEQAKMDHGRDQFLRHPVCSQSKLE 60  
 DB 18 RSMCFGLVLYGLLYLVFAGAVSSVLPYEDLLRDLRLKRLKRFLEHHCLESEQQLD 77

```

QY 61 FIKLIVLALGCG---ANPETSMTNSSNHSANLGSAPFPSCGTTITIGNVLHTDA 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 FLGRVLEASNYGVSLVSNAGNMN-----WDFTSALFPASTVSTIGTGTVPLSDG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 GRFCFCFYALVGIPLFGMLLAGVDRIGSSL-RRIGIHIEALFLKWHVPPGLVRSLSAVL 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 GKAFCLITVSVIGPFLFLFTAVQRIYVTRRPVLYFH---IRMGFSKVQVAVIHAVL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 -FLIGCLLEFLVLPFPFSYME-SMSKLEAIYFVITLTGFGDYGSDGTGON-SPA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 LGEFVVSCEFFI--PAAVSVLEDDMNLFESFPCISLTIGLGDYVPEGYNOKFREL 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 YQPLVWFVWLFGLAFVAVLT 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 YKIGTCYLLGLLTMVLVLET 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
C1W1_MOUSE STANDARD; PRT; 336 AA.
ID C1W1_MOUSE
AC 008581;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 1 (Inward rectifying potassium
   channel protein TWIK-1).
GN KCNK1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97165959; PubMed=9013852;
RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
   Lqduński M.;
RT "The structure, function and distribution of the mouse TWIK-1 K+
   channel";
RL FEBS Lett. 402:28-32(1997).
   [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RX MEDLINE=98218573; PubMed=955671;
RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barbanin J.;
RT "Structure, chromosome localization, and tissue distribution of the
   mouse twik K+ channel gene";
RL FEBS Lett. 425:310-316(1998).
   [3]
CC -FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -SUBUNIT: HOMODIMER (POTENTIAL).
CC -SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
   KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
   EPIDIDYMIS, UTERUS, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
   OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
   MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
   CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
   CORTEX.
CC -DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
   CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
   STABILIZES AFTER DAY 8.
CC -MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
   ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
   CHANNELS.
CC -----
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CC -----
CC EMBL: AF033017; AAC16973.1;
CC MGD: MGI:109322; Kcnk1.
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_1ig.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PRO1333; 2PORECHANNEL.
DR PRINTS: PRO1096; TWIK1CHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

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Query Match 17.8%; Score 369.5; DB 1; Length 336;
Best Local Similarity 34.0%; Pred. No. 1.4e-13;
Matches 89; Conservative 53; Mismatches 97; Indels 23; Gaps 9;

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```

QY 2 RSTTLALAL-VLTVLSAIVFOALBOPHDOAKKRDGDFLNDHPVCSOKSLSD 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 RSAMWCGFLVGLTVLGVAVFSSSELPYEDLRKRLKRRLEHESLSEPOLEQ 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 FIKLIVLALGCG---ANPETSMTNSSNHSANLGSAPFPSCGTTITIGNVLHTDA 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 FLGRVLEASNYGVSLVSNAGNMN-----WDFTSALFPASTVSTIGTGTVPLSDG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 GRFCFCFYALVGIPLFGMLLAGVDRIGSSL-RRIGIHIEALFLKWHVPPGLVRSLSAVL 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 GKAFCLITVSVIGPFLFLFTAVQRIYVTRRPVLYFH---IRMGFSKVQVAVIHAVL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 -FLIGCLLEFLVLPFPFSYME-SMSKLEAIYFVITLTGFGDYGSDGTGON-SPA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 LGEFVVSCEFFI--PAAVSVLEDDMNLFESFPCISLTIGLGDYVPEGYNOKFREL 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 YQPLVWFVWLFGLAFVAVLT 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 YKIGTCYLLGLLTMVLVLET 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
ORK1_DROME STANDARD; PRT; 1001 AA.
ID ORK1_DROME
AC 094526;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Open rectifier potassium channel protein 1 (Two pore domain potassium
   channel Ork1).
GN ORK1 OR CG1615.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridioidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larva;
RX MEDLINE=97075152; PubMed=8917578;
RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.;
RT "ORK1, a potassium-selective leak channel with two pore domains
   cloned from Drosophila melanogaster by expression in Saccharomyces

```

Query Match	Best Local Similarity	Score	DB 1	Length
Matches 95; Conservative 54; Mismatches 104; Indels 74; Gaps 9;	29.1%; Pred. No. 3.1e-12;	353;	DB 1;	1001;
7 LALLALVLLVYSGALVQALEQHPHEQQAQKKMDGRQFLRDHCVCQKSLDEPIKLLV 66	7 LALLALVLLVYSGALVQALEQHPHEQQAQKKMDGRQFLRDHCVCQKSLDEPIKLLV 66			
7 ILLLFYSLYLMFGAIIYHIE-----HGEKISRAEQRQAIAINEV--LL 51	7 ILLLFYSLYLMFGAIIYHIE-----HGEKISRAEQRQAIAINEV--LL 51			
67 EALGG-----ANPETSMTNSNHSAMNLSGAFESGFTITTTGYGNI 110	67 EALGG-----ANPETSMTNSNHSAMNLSGAFESGFTITTTGYGNI 110			
52 EELGCKNTTQDELLIQRISDCDKRVTLTPRYDDIPRYTWYTHAFEFYTCVGYGNI 111	52 EELGCKNTTQDELLIQRISDCDKRVTLTPRYDDIPRYTWYTHAFEFYTCVGYGNI 111			
111 VLHDTAGRLFCIFVALVGIPLFGMLLAGVDRGLSSLRIGIHTEAIFLK----- 161	111 VLHDTAGRLFCIFVALVGIPLFGMLLAGVDRGLSSLRIGIHTEAIFLK----- 161			
112 SPFTAGRMIMIAVSVIGIPVNGILFAGLGEYFRT-----FEAIRRKYKMYSTM 164	112 SPFTAGRMIMIAVSVIGIPVNGILFAGLGEYFRT-----FEAIRRKYKMYSTM 164			
162 -HYPPGLVRLSAVLFLLIGCLLPVLPFPFVSYSKSLKELAIYFVLTLTGFGGY 220	162 -HYPPGLVRLSAVLFLLIGCLLPVLPFPFVSYSKSLKELAIYFVLTLTGFGGY 220			
165 HYPPGLDITTTVITALPGIALFLLPSWPFYFENMPYSISLYSVTTTIGFGDY 224	165 HYPPGLDITTTVITALPGIALFLLPSWPFYFENMPYSISLYSVTTTIGFGDY 224			
221 PDGGGQNSP-----AYQPLWFMFLGLFAVFSVLTITGNMLRAVSRRTAEKGLTA 274	221 PDGGGQNSP-----AYQPLWFMFLGLFAVFSVLTITGNMLRAVSRRTAEKGLTA 274			
225 PTFGANGKREKGGMVFVQIFVYWFIFISLGLVIMMFIIRGLS-----KRLAYLEQ 278	225 PTFGANGKREKGGMVFVQIFVYWFIFISLGLVIMMFIIRGLS-----KRLAYLEQ 278			
275 QAAS-----WTGVTARVYRTQRTG 292	275 QAAS-----WTGVTARVYRTQRTG 292			
279 QLSMLKATQNKRMWG-----VTKDVG 300	279 QLSMLKATQNKRMWG-----VTKDVG 300			
RESULT 12				
CIW9_CAVPO	CIW9_CAVPO			
CIW9_CAVPO	CIW9_CAVPO			
9QJL58:	9QJL58:			
16-OCT-2001 (Rel. 40, Created)	16-OCT-2001 (Rel. 40, Created)			
16-OCT-2001 (Rel. 40, Last sequence update)	16-OCT-2001 (Rel. 40, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update)	16-OCT-2001 (Rel. 40, Last annotation update)			
Potassium channel subfamily K member 9 (Acid-sensitive potassium	Potassium channel subfamily K member 9 (Acid-sensitive potassium			
channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).	channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).			
KCNK9 OR TASK3.	KCNK9 OR TASK3.			
Cavia porcellus (Guinea pig).	Cavia porcellus (Guinea pig).			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
NCBI_Taxid:10141;	NCBI_Taxid:10141;			
[1]	[1]			
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			
TISSUE=Brain.	TISSUE=Brain.			
MEDLINE=20287530; PubMed=10747866;	MEDLINE=20287530; PubMed=10747866;			
Rajan S., Mischneyer E., Liu G.X., Preisig-Mueller R., Daut J.,	Rajan S., Mischneyer E., Liu G.X., Preisig-Mueller R., Daut J.,			
Karschn A., Derst C.;	Karschn A., Derst C.;			
"TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An	"TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An			
extracellular histidine as pH sensor.";	extracellular histidine as pH sensor.";			
J. Biol. Chem. 275:16650-16657(2000)."	J. Biol. Chem. 275:16650-16657(2000)."			
-1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM	-1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM			
CHANNEL, PROTEIN.	CHANNEL, PROTEIN.			
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM			
CHANNELS.	CHANNELS.			
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DR EMBL: AF212827; AAF63706.1; -  
DR InterPro: IPR003280; 2porek\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR003092; TASK\_channel.  
DR Pfam: PF00520; Ion\_trans.1.  
DR PRINTS: PR01333; 2POREKCHANEL.  
DR PRINTS: PR01095; TASKCHANNEL.  
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
KW Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 POTENTIAL.  
FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
FT TRANSMEM 108 128 POTENTIAL.  
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
FT TRANSMEM 219 239 POTENTIAL.  
FT DOMAIN 240 365 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 365 AA; 40769 MW; 261DC973FE53AF91 CRC64;

Query Match 16.0%; Score 333.5; DB 1; Length 365;  
Best Local Similarity 28.3%; Pred. No. 1.3e-11;  
Matches 104; Conservative 55; Mismatches 124; Indels 85; Gaps 12;

QY 7 LALLALVLYVSGALVFAQLBEPHQQAQKMDHGRDPLRHPVCSQR---SLEDFIK 63  
DB 9 LSLIACTFTYLLVGAALVFAQLBEPHQQAQKMDHGRDPLRHPVCSQR---SLEDFIK 61  
QY 64 LVEALGSGANPEPSTWNTSSNHSNA--WNLSAFAFFSGTITITIGYGVNLTADAGLFC 121  
DB 62 LELVIL-----QSPHRAGVQWKRKAGSFYFAITVITITIGYGVNLTADAGLFC 110  
QY 122 IFYALVGLPFLGMLAGVGRGSLRIGITIAIFLKMHPVPGVLVRSALVFLIGC 181  
DB 111 MEYALVGLPFLGMLAGVGRGSLRIGITIAIFLKMHPVPGVLVRSALVFLIGC 170  
QY 182 LLEVLITFEVSMESKLEATYVLTITVYFGDYV--PEDGTGQNSPAQPLVWFM 239  
DB 171 LCI---GAAAFSGCEMSEFPHAYVCTITLTITIGFDYVALQSGKALQKRPVAVSFMY 227  
QY 240 ILFGLAVF-----ASVLTITIGMLRAVSRRT 266  
DB 228 ILVGLVIGAFNLVYLRFLTMSDSEGESEGAALPGNPSVYVHISEAQQVRRYR 287  
QY 267 AEMGGLTAQAASGTGVTARVORTGPS-----APPE-----KEOPLIPSSL-----P 310  
DB 288 GREGDILQ-----SVSCACYRSPQPNFGATLAPQPLHSICRIEISPSLKNLSLP 339  
QY 311 APPAVPEP 318  
DB 340 SPISVSP 347

RESULT 13  
CIV3\_MOUSE  
ID CIV3\_MOUSE STANDARD: PRT; 409 AA.  
AC 035111; 035163;  
DT 16-OCT-2001 (Rel. 40; Created)  
DT 16-OCT-2001 (Rel. 40; Last sequence update)  
DT 16-OCT-2001 (Rel. 40; Last annotation update)  
DE Potassium channel subfamily K member 3 (acid-sensitive potassium  
DE channel protein TASK) (TWIK-related acid-sensitive K+ channel)  
DE (Cardiac two-pore background K+ channel) (CTBAK-1).  
GN KCNK3 OR TASK OR CTBAK.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=98165556; PubMed=9506712;  
RT Kim D., Fujita A., Horio Y., Kurachi Y.;  
RT "Cloning and functional expression of a novel cardiac two-pore  
RT background K+ channel (CTBAK-1).";  
RL Circ. Res. 82:513-518(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=20287574; PubMed=10748056;  
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;  
RT "Proton block and voltage gating are potassium-dependent in the  
RT cardiac leak channel Kcnk3.";  
RL J. Biol. Chem. 275:16969-16978(2000).  
RN [3]  
RP SEQUENCE OF 4-409 FROM N.A.  
RX MEDLINE=97459932; PubMed=9312005;  
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
RT "TASK, a human background K+ channel to sense external pH variations  
RT near physiological pH.";  
RL EMO J. 16:5464-5471(1997).  
CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE. BACKGROUND POTASSIUM  
CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM  
CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD  
CC (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED  
CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL  
CC INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.  
CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.  
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
CC CHANNELS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: AB008537; BAA25436.1; -  
EMBL: AF241798; AAF81418.1; -  
EMBL: AF242508; AAF81418.1; JOINED.  
EMBL: AF065162; AAG29339.1; -  
EMBL: AF006824; AAC53367.1; -  
EMBL: AB013345; BAA28349.1; -  
MGI: MGI:1100509; Kcnk3.  
DR InterPro: IPR003280; 2porek\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR003092; TASK\_channel.  
DR Pfam: PF00520; Ion\_trans.1.  
DR PRINTS: PR01333; 2POREKCHANEL.  
DR PRINTS: PR01095; TASKCHANNEL.  
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
KW Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 POTENTIAL.  
FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
FT TRANSMEM 108 128 POTENTIAL.  
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

FT TRANSMEM 223 243 POTENTIAL.  
 FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 4 4 Q -> E (IN REF. 3).  
 FT CONFLICT 123 123 V -> I (IN REF. 3).  
 SO SEQUENCE 409 AA; 45068 MW; 35236E01AAC5687 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 409;  
 Best Local Similarity 31.6%; Pred. No. 1.7e-11;  
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

7 LALLALVILVLSGALVFPALPQHPHQAKKNDGRQFLRPHPCVSKSLIEDFKLLV 66  
 9 LALLVCTFTLLVGAVFDALESEPEMERORLEL-ROLELRARYNLSEGYEELERVVL 67  
 67 EALGGANPETSWTNSNHSAMNLGSAFFSGTITITIGYNIYLHTDAGRLFCIFYAL 126  
 68 RLKPKHAGVQ-----WRFAGSFYFAITVITITIGYHAPSDGKVFCEFYAL 115  
 127 VGIPLEGMLAGVDRGLSSLR-----RGIG--HIEAIFLKNVHPGGLVRSLSAVLEL 177  
 116 LGIPFLVLFQSLGERINTEFVRLHLRAKRGIGMRHAE-----VSMANVLLIG 163  
 178 LIGCLLFVLTPTFVFSYMSKLEAIFYVITLTVGGDYY--PGDGTGNSPAYOPL 235  
 164 FVSCISTLCIGAALFSTYERWTFQAYVYCFITLITIGRDYVALQKDALQOTPOY--- 220  
 236 VWFMIIFGLAYFASVLTITGNMLRAVSR 264  
 221 ----VAFSFVYILTGLTVIGAFNLVLR 245

RESULT 14  
 C1W3\_RAT  
 ID C1W3\_RAT STANDARD; PRT; 411 AA.  
 AC 054912;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).  
 GN KCKN3 OR TASK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=98099797; PubMed=9437008;  
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;  
 RA "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum";  
 RT J. Neurosci. 18:868-877(1998).  
 RL J. Neurosci. 18:868-877(1998).  
 CC -1- FUNCTION: PH-DEPENDENT VOLTAGE-INSENSITIVE BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.  
 CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BOPIVACAIN AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF031384; AAC39952.1; -  
 DR InterPro: IPR003280; 2porek channel.  
 DR InterPro: IPR000636; Cation\_chan\_nou\_119.  
 DR InterPro: IPR001622; Channel\_pore\_K.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 DR PRINTS: PR01095; TASKCHANNEL.  
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.  
 KW DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 108 128 POTENTIAL.  
 FT TRANSMEM 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 223 243 POTENTIAL.  
 FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 411 AA; 45276 MW; D278016E09E2B5 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 411;  
 Best Local Similarity 31.6%; Pred. No. 1.7e-11;  
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

7 LALLALVILVLSGALVFPALPQHPHQAKKNDGRQFLRPHPCVSKSLIEDFKLLV 66  
 9 LALLVCTFTLLVGAVFDALESEPEMERORLEL-ROLELRARYNLSEGYEELERVVL 67  
 67 EALGGANPETSWTNSNHSAMNLGSAFFSGTITITIGYNIYLHTDAGRLFCIFYAL 126  
 68 RLKPKHAGVQ-----WRFAGSFYFAITVITITIGYHAPSDGKVFCEFYAL 115  
 127 VGIPLEGMLAGVDRGLSSLR-----RGIG--HIEAIFLKNVHPGGLVRSLSAVLEL 177  
 116 LGIPFLVLFQSLGERINTEFVRLHLRAKRGIGMRHAE-----VSMANVLLIG 163  
 178 LIGCLLFVLTPTFVFSYMSKLEAIFYVITLTVGGDYY--PGDGTGNSPAYOPL 235  
 164 FVSCISTLCIGAALFSTYERWTFQAYVYCFITLITIGRDYVALQKDALQOTPOY--- 220  
 236 VWFMIIFGLAYFASVLTITGNMLRAVSR 264  
 221 ----VAFSFVYILTGLTVIGAFNLVLR 245

RESULT 15  
 C1W9\_HUMAN  
 ID C1W9\_HUMAN STANDARD; PRT; 374 AA.  
 AC 09NRC2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).  
 GN KCKN9 OR TASK3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20287530; PubMed=10747866;  
 RA Rajan S., Mischmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Dierck C.;

RT "TASK-3", a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An  
RT extracellular histidine as pH sensor.";  
RL J. Biol. Chem. 275:16650-16657(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cerebellum;  
RX MEDLINE=20499203; PubMed=11042359;  
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
RA Kelsell R.E., Muddock P.R., Randall A.D., Rennie G.I., Gloger I.S.;  
RT "Cloning, localisation and functional expression of a novel human,  
RT cerebellum specific, two pore domain potassium channel.";  
RL Brain Res. Mol. Brain Res. 82:74-83(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Girard C., Lesage F., Tinel N., Lazdunski M.;  
RT "Human Task-3, a novel 2p domain potassium channel related to Task.";  
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,  
RA Coetzee W., Rudy B.;  
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
CC -I- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
CC CHANNEL PROTEIN.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
CC -I- TISSUE SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.  
CC -I- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
CC CHANNELS.  
CC -----  
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CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
CC -----  
DR EMBL: AF212829; AAF63708.1; -  
DR EMBL: AF248241; AAG31730.1; -  
DR EMBL: AF279809; AAF85982.1; -  
DR EMBL: AF257080; AAG33126.1; -  
DR MIM: 605874; -  
DR InterPro: IPR003280; 2poreK\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR003092; TASK\_channel.  
DR Pfam: PF00520; Ion\_trans\_1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01095; TASKCHANNEL.  
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
KW Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 POTENTIAL.  
FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
FT TRANSMEM 108 128 POTENTIAL.  
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
FT TRANSMEM 219 239 POTENTIAL.  
FT DOMAIN 240 374 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
FO SEQUENCE 374 AA; 42263 MW; 8A19EAE5A4D7F38 CRC64;

Query Match 15.8%; Score 327.5; DB 1; Length 374;  
Best Local Similarity 28.7%; Pred. No. 2.9e-11;  
Matches 107; Conservative 54; Mismatches 147; Indels 65; Gaps 13;

QY 7 LALLALVLLVSGALVEQALPEHQQAOKKMDGRDQFLRDHPVCSQK--SLDFIK 63  
DB 9 LSLIVCTFTYLLVGAALVDALSDHEMRREKTL--KAKEIR----IKKYNISSEDDYRQ 61  
QY 64 LLVEALGGANPETSWTSSNHSNA--WNLGSAFFFGTIIITTYGNIIVLHTDAGRLFC 121

DB 62 LELVIL-----QSEPHRAGYQWKFAGSFYTAIVTITIGYGHAPGTDAKAF 110  
QY 122 IFYALVGLPFCMLLAGVDRGLSSLRIGITAEIFLKWHVPPGLVRSLSAVLFLLLIG 181  
DB 111 MFYAVIGIFLLVMFQSLGERMTEFVRLKRIKCCGMNNTDVSMMNVTVGFFSCMG 170  
QY 182 LLEVLPTVEFSVMESKMLEATFYIVLTYVGFDDY--PDGTGQNSPAQPLVYMW 239  
DB 171 LCI---GAAAFSCQERMSFFHAYTCITLTYTGFDYVALQTKGALOKKPLVAFSEW 227  
QY 240 ILFGLAFFASVLTITGNWLRV-----SRRTAEIMGILTQAASMTGTVART 288  
DB 228 ILVG-----LTVIGAFILNIVLRLFMNSEDERRDAERASLACNRNS---MYIHIP 276  
QY 289 QRTGSAPEPEKEQPLPSLPAP-PAYVEPAGRGSP-----AP-----AEKVET 333  
DB 277 EEPREPSPRYKADVPLQSGVSCQCYRSODYGGRSVAPONSFSAKLAPHYFHSISYKIE 336  
QY 334 PSPPTASALDPS 346  
DB 337 ISPTLKNLSPS 349

Search completed: June 4, 2002, 11:03:40  
Job time: 204 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:56:40 : Search time 31.63 Seconds  
(without alignments)  
1397.641 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079

Sequence: 1 MRSTLLALALVLLVLSG.....SKKRPSPGPGRLKAVPV 398

Scoring table:

BLOSUM62  
Gapop 10.0, Gapect 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq\_032802:\*

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2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

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19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

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22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	100.0	398	20	AAV30647
2	1692.5	81.4	393	21	AAV94425
3	1692.5	81.4	393	21	AAV94426
4	1692.5	81.4	393	22	AAV67777
5	1688.5	81.2	1314	22	AAV04571
6	895	43.0	421	22	AAV12229
7	776.5	37.3	411	20	AAV34133
8	776.5	37.3	411	20	AAV28496
9	776.5	37.3	411	21	AAE10341
10	776.5	37.3	411	22	AAV50044
11	770.5	37.1	370	20	AAV30648

12	770.5	37.1	411	20	AAV28497
13	770.5	37.1	411	21	AAE10342
14	759.5	36.5	426	22	AAV07618
15	755.5	36.3	426	22	AAV07622
16	754.5	36.3	426	22	AAV07623
17	753.5	36.2	426	22	AAV07624
18	751.5	36.1	426	22	AAV07625
19	427.5	20.6	332	22	AAE01027
20	427.5	20.6	332	22	AAE01027
21	416	20.0	499	21	AAV94875
22	416	20.0	499	21	AAV94875
23	416	20.0	499	22	AAE01026
24	416	20.0	511	22	AAV24148
25	397.5	18.1	155	22	AAV4132
26	397.5	18.1	155	20	AAV4132
27	386	18.6	313	20	AAV5116
28	386	18.6	313	20	AAV5116
29	386	18.6	313	21	AAV0355
30	386	18.6	313	21	AAV68737
31	386	18.6	313	21	AAV68738
32	386	18.6	313	22	AAE01028
33	379.5	18.3	336	21	AAV79673
34	379.5	18.3	336	22	AAV79673
35	377.5	18.2	383	22	AAV02731
36	361.5	17.4	1001	22	AAV31805
37	353	17.0	107	20	AAV58298
38	343	16.5	107	20	AAV58298
39	332.5	16.0	405	21	AAV95230
40	327.5	15.8	374	21	AAV18807
41	327.5	15.8	374	21	AAV18813
42	327.5	15.8	374	22	AAV63938
43	326.5	15.7	394	21	AAE10343
44	326.5	15.7	394	21	AAV79674
45	326.5	15.7	394	21	AAV87291

#### ALIGNMENTS

RESULT	ID	AAV30647	standard; Protein: 398 AA.
XX	AC	AAV30647:	
XX	DT	18-NOV-1999	(first entry)
XX	DE	A mechanically sensitive potassium channel protein TRAK.	
XX	KW	Mechanically sensitive potassium channel protein; TRAK;	
XX	KW	polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;	
XX	KW	nervous system disease; epilepsy; cardiovascular disease; arrhythmia;	
XX	KW	neurodegeneration; ischemia; anoxia; hormone secretion abnormality;	
XX	KW	muscular disease.	
XX	OS	Mus sp.	
XX	PN	WO9945108-A2.	
XX	PD	10-SEP-1999.	
XX	PF	23-FEB-1999;	99WO-FR00404.
XX	PR	05-MAR-1998;	98FR-0002725.
XX	PA	(CNRS ) CNRS CENT NAT RECH SCI.	
XX	PT	Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;	
XX	DR	WPI: 1999-551038/46.	
XX	PT	N-PSDB: AA210606.	
XX	PT	New mechanically sensitive potassium channel, used to screen for	

Mouse h-TREK1 poly  
Murine TREK-1 pota  
Human potassium io  
Human potassium io  
Human potassium io  
Human potassium io  
Human TREK-3 prote  
Human TREK-2 prote  
Human potassium clon  
Human protein clon  
Human TREK-2 prote  
Novel human diagno  
Human EST encoded  
Human potassium ch  
Human hTREK-1 prot  
Human TREK-4 prote  
KT4, a TWIK family  
TWIK, a TWIK family  
Human TWIK-4 prote  
Human TWIK-1 potass  
Human potassium c  
Human human diagno  
Novel human diagno  
Amilo acid sequenc  
Drosophila melanog  
Partial h-TREK1 po  
Mouse potassium ch  
Amino acid sequenc  
Protein encoded by  
Amino acid sequenc  
Murine TASK potass  
Human potassium ch  
Human signal pepti



PT specific modulators, potential therapeutic agents for heart and nervous  
 XX system disorders  
 PS Claim 2; Fig 1; 40pp; French.

XX The present sequence represents a mechanistically sensitive potassium  
 CC channel protein designated TPAK. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.  
 XX Sequence 398 AA;

Query Match 100.0%; Score 2079; DB 20; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 4e-169;  
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSTLLALALVLLVLSGALVFOALPQHPQOAKKMDHGRQFLRDHPVCSQKSLSD 60  
 Db 1 msttllallalvllvlsгалvfoalpqhpoakkmhgrqflrdhpcvsqksled 60  
 QY 61 FIKLVEALGGANPETSWTSSNNSSNWSNMGSAFFSGTITTTIGXGNVLTHTDAGRLF 120  
 Db 61 fklvlealgganpetswtssnnssnwsnmgasaffsgtitttlygnvlthtdagrlf 120  
 QY 121 CIFVYALGIPLFQMLLAGVSDRLGSSLRGIGHEATFLKWHVPPGLVNSLSAVLFLTLG 180  
 Db 121 cifvyalgipflfqmltagvsgdrlgsslsrgighetflkwhvppglvnslsavfltlg 180  
 QY 181 CLLEVLPTFFVFSYMSKLEATFYVTLTVGFGDYVPGGCTGONSAPATOPVWMT 240  
 Db 181 cllevlptffvfymseskleatfyvltvtvgfgdyvpggctgonsapatoptvwm 240  
 QY 241 LFGATVFAVYTTTIGNMLRAVSRRTRAEMGGLTAQAASWTGVTARVQRTGPSAPPEK 300  
 Db 241 lfgatvfasvtttignmlravssrrtraemggltaqaaawtgvtarvqrtgpsappek 300  
 QY 301 EQLLPSSLPAPVAVVEPAGRGSPAPPAKVTBSPPTASALDYPSENIAFIDESSPTOS 360  
 Db 301 eqllpsslpapvavvepagspapekvtbbspptasaldypseniafidessptos 360  
 QY 361 ERGCLPRAPRGRRRPNPSKPSRPRGRLRDKAVPV 398  
 Db 361 ergclpraprrtrppskpsrprgrlrdkavpv 398

RESULT 2  
 AAY94425  
 ID AAY94425 standard; Protein: 393 AA.  
 AC XX  
 XX AAY94425;  
 DT 04-AUG-2000 (first entry)  
 DE XX  
 XX Human h-TPAK polypeptide #1.  
 KW Human; h-TPAK; potassium channel polypeptide;  
 KW 2p domain potassium channel; neurodegenerative disease; stroke;  
 XX psychiatric disorder; neurological disorder; Gene therapy.  
 OS Homo sapiens.  
 XX  
 PN W0200026253-A1.  
 XX  
 PD 11-MAY-2000.  
 XX

11-MAY-2000.

PF 03-NOV-1999; 99WO-GB03634.  
 XX  
 XX  
 PR 03-NOV-1998; 98GB-0024048.  
 PR 07-OCT-1999; 99GB-0023668.  
 XX  
 PA (SMIR) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Chapman CG, Duckworth DM;  
 XX  
 DR WPI: 2000-365583/31.  
 DR N-PSDB: AAA27105.  
 XX  
 PT Novel isolated h-TPAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of  
 PT h-TPAK related disorders, e.g. depression and schizophrenia  
 XX  
 PS Claim 3; Page 21; 35pp; English.

XX Functional genomics was used to identify h-TPAK polypeptides and  
 CC h-TPAK polynucleotides from human tissue samples. h-TPAK  
 CC polypeptides have homology to the 2p domain potassium channel family of  
 CC polypeptides. The h-TPAK polypeptides and polynucleotides may  
 CC be used in diagnostic assays for conditions related to h-TPAK  
 CC imbalance and for identifying agonists and antagonists of h-TPAK  
 CC polypeptides. The h-TPAK polypeptides and polynucleotides may also  
 CC be useful for treatment and prevention (e.g. as vaccines) of certain  
 CC diseases, such as pain, psychiatric disorders including depression and  
 CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke  
 CC and head trauma and neurological disorders including migraine and  
 CC epilepsy. The present sequence is human h-TPAK protein #1.  
 XX Sequence 393 AA;

Query Match 81.4%; Score 1692.5; DB 21; Length 393;  
 Best Local Similarity 82.4%; Pred. No. 3.8e-136;  
 Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;

QY 1 MRSSTLLALALVLLVLSGALVFOALPQHPQOAKKMDHGRQFLRDHPVCSQKSLSD 60  
 Db 1 msttllallalvllvlsгалvfoalpqhpoakkmhgrqflrdhpcvsqksled 60  
 QY 61 FIKLVEALGGANPETSWTSSNNSSNWSNMGSAFFSGTITTTIGXGNVLTHTDAGRLF 120  
 Db 61 fklvlealgganpetswtssnnssnwsnmgasaffsgtitttlygnvlthtdagrlf 120  
 QY 121 CIFVYALGIPLFQMLLAGVSDRLGSSLRGIGHEATFLKWHVPPGLVNSLSAVLFLTLG 180  
 Db 121 cifvyalgipflfqmltagvsgdrlgsslsrgighetflkwhvppglvnslsavfltlg 180  
 QY 181 CLLEVLPTFFVFSYMSKLEATFYVTLTVGFGDYVPGGCTGONSAPATOPVWMT 240  
 Db 181 cllevlptffvfymseskleatfyvltvtvgfgdyvpggctgonsapatoptvwm 240  
 QY 241 LFGATVFAVYTTTIGNMLRAVSRRTRAEMGGLTAQAASWTGVTARVQRTGPSAPPEK 300  
 Db 241 lfgatvfasvtttignmlravssrrtraemggltaqaaawtgvtarvqrtgpsappek 300  
 QY 301 EQLLPSSLPAPVAVVEPAGRGSPAPPAKVTBSPPTASALDYPSENIAFIDESSPTOS 360  
 Db 301 eqllpsslpapvavvepagspapekvtbbspptasaldypseniafidessptos 360  
 QY 361 ERGCLPRAPRGRRRPNPSKPSRPRGRLRDKAVPV 398  
 Db 361 ergclpraprrtrppskpsrprgrlrdkavpv 398

RESULT 3  
 AAY94426  
 ID AAY94426 standard; Protein: 393 AA.  
 AC XX  
 XX AAY94426;  
 DT 04-AUG-2000 (first entry)  
 DE XX  
 XX Human h-TPAK polypeptide #1.  
 KW Human; h-TPAK; potassium channel polypeptide;  
 KW 2p domain potassium channel; neurodegenerative disease; stroke;  
 XX psychiatric disorder; neurological disorder; Gene therapy.  
 OS Homo sapiens.  
 XX  
 PN W0200026253-A1.  
 XX  
 PD 11-MAY-2000.  
 XX



DT 04-AUG-2000 (first entry)

XX Human h-TRAAK polypeptide #2.

DE Human: h-TRAAK, potassium channel polypeptide;

KW 2p domain potassium channel; neurodegenerative disease; stroke;

KW psychiatric disorder; neurological disorder; Gene therapy.

XX Homo sapiens.

OS WO200026253-A1.

PN 11-MAY-2000.

PD 03-NOV-1999; 99MO-GB03634.

PF 03-NOV-1998; 98GB-0024048.

PR 07-OCT-1999; 99GB-0023668.

XX (SMK) SMITHKLINE BEECHAM PLC.

PA Chapman CG, Duckworth DM;

PI WPI: 2000-365583/31.

XX N-PSDB: AAA27106.

DR Novel isolated h-TRAAK polypeptides belonging to the potassium channel

PT family of polypeptides, useful for the diagnosis and treatment of

PT h-TRAAK related disorders, e.g. depression and schizophrenia -

XX Claim 12; Pages 21 and 22; 35pp; English.

PS Functional genomics was used to identify h-TRAAK polypeptides and

XX h-TRAAK polynucleotides from human tissue samples. h-TRAAK

CC polypeptides have homology to the 2p domain potassium channel family of

CC polypeptides. The h-TRAAK polypeptides and polynucleotides may

CC be used in diagnostic assays for conditions related to h-TRAAK

CC imbalance and for identifying agonists and antagonists of h-TRAAK

CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also

CC be useful for treatment and prevention (e.g. as vaccines) of certain

CC diseases, such as pain, psychiatric disorders including depression and

CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke

CC and head trauma and neurological disorders including migraine and

XX epilepsy. The present sequence is human h-TRAAK protein #2.

XX Sequence 393 AA;

SO

Query Match 81.4%; Score 1692.5; DB 21; Length 393;

Best Local Similarity 82.4%; Pred. No. 3.8e-136;

Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;

DB 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

QY 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

DB 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

QY 61 FIKLVEALGGANPESWTSSNHSNMGSAFFSSGRTITIGNIVLHTDARLF 120

DB 61 FIKLVEALGGANPESWTSSNHSNMGSAFFSSGRTITIGNIVLHTDARLF 120

QY 61 LKVEDALGGADPETSNSH-SAWDLSGSAFFSGLTILTYGNAVALLRDAQRL 119

DB 61 LKVEDALGGADPETSNSH-SAWDLSGSAFFSGLTILTYGNAVALLRDAQRL 119

QY 121 CIFVALVGLPFGMLLAGDRLGSLRRGIGHTEAIFLKMHPVPGVLSLAVFLILG 180

DB 121 CIFVALVGLPFGMLLAGDRLGSLRRGIGHTEAIFLKMHPVPGVLSLAVFLILG 180

QY 120 CIFVALVGLPFGMLLAGDRLGSLRRGIGHTEAIFLKMHPVPGVLSLAVFLILG 179

DB 120 CIFVALVGLPFGMLLAGDRLGSLRRGIGHTEAIFLKMHPVPGVLSLAVFLILG 179

QY 181 CLFLVLPTEFVSYSMSKLEAIFVYVTLTTFVGFYVGDGCGNSPAYOPVPMFMI 240

DB 181 CLFLVLPTEFVSYSMSKLEAIFVYVTLTTFVGFYVGDGCGNSPAYOPVPMFMI 240

QY 180 CLFLVLPTEFVSYSMSKLEAIFVYVTLTTFVGFYVGDGCGNSPAYOPVPMFMI 239

DB 180 CLFLVLPTEFVSYSMSKLEAIFVYVTLTTFVGFYVGDGCGNSPAYOPVPMFMI 239

QY 241 LFLGLAVASVLTIGMIRAVSRRTAEEMGGLTAQAASTGVTARVOTQRTGPSAPPEK 300

DB 241 LFLGLAVASVLTIGMIRAVSRRTAEEMGGLTAQAASTGVTARVOTQRTGPSAPPEK 300

QY 240 LFLGLAVASVLTIGMIRAVSRRTAEEMGGLTAQAASTGVTARVOTQRTGPSAPPEK 299

DB 240 LFLGLAVASVLTIGMIRAVSRRTAEEMGGLTAQAASTGVTARVOTQRTGPSAPPEK 299

QY 301 EOPILPSLPAVPAVVEPAGPGSPAPAEKVTPTASALDYSENLAIFIDESSDROS 360

DB 301 EOPILPSLPAVPAVVEPAGPGSPAPAEKVTPTASALDYSENLAIFIDESSDROS 360

DB 300 exp1----lpppcpapiygrtspsppekagppspclasadldypsenlafidesdts 355

QY 361 ERGCALPRAPGRRRPNPSKKPSRPRGRLRDKAVPV 398

DB 356 ergcpiprprgrtrrrppppkpvrrpgrpgrdkgyvpv 393

RESULT 4

AA67777

ID AA67777 standard; Protein; 393 AA.

XX AA67777;

AC AA67777;

XX 10-DEC-2001 (first entry)

DT Human mechanically sensitive potassium channel hTRAAK polypeptide.

DE Human: mechanically sensitive potassium channel; riluzole; TWICK;

XX polynunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;

KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;

KW hormone secretion; cardiac disease; vascular disease; ischemia;

KW nervous system disorder; endocrinal disease; muscle disease;

KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration.

XX Homo sapiens.

OS WO200168670-A2.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-FR00758.

XX 14-MAR-2000; 2000FR-0003264.

PR (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Maingret F;

PI WPI: 2001-590037/66.

XX N-PSDB: AAH78636, AAH78646.

DR New mechanically sensitive potassium channel, useful for treating

PT cardiovascular diseases and in drug screening, is activated by

PT polynunsaturated fatty acids -

XX Claim 1; Page 34-35; 37pp; French.

PS The present sequence represents a human mechanically sensitive potassium

XX channel which is activated by polynunsaturated fatty acids (particularly

CC arachidonic acid (AA)) and by riluzole. The polypeptide is designated

CC human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK

CC gene is located on chromosome 11q13. hTRAAK is involved in regulation

CC of neuronal and muscle excitation, cardiac rhythm and secretion of

CC hormones. Cells that express hTRAAK, designated to screen for modulators

CC of hTRAAK activity. Such modulators are potentially useful for prevention

CC or treatment of human and animal, of: cardiac and/or vascular disease;

CC nervous system disorders associated with ischemia and anoxia; endocrinal

CC diseases associated with anomalous hormone secretion or muscle diseases;

CC and retinal diseases. Typical examples are epilepsy, cardiac arrhythmia

XX and neurodegeneration.

XX Sequence 393 AA;

SO

Query Match 81.4%; Score 1692.5; DB 22; Length 393;

Best Local Similarity 82.4%; Pred. No. 3.8e-136;

Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;

DB 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

QY 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

DB 1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMDHGRDQFLRDHPCVQSQSLSD 60

**Claim 10:** Page 203-208; 259pp: English.

The sequence represents a human G-protein coupled receptor (GPCR)-like protein found to be homologous to human h-TFAK polypeptide #1. The GPCR-like polypeptides and polynucleotides are useful for disease and Parkinson's disease, immunological (e.g HIV infection and candidiasis), autoimmune disorders (e.g multiple sclerosis, systemic lupus erythematosus and rheumatoid arthritis) platelet disorders (e.g thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g septic shock and systemic inflammatory response syndrome, SIRS) and nephritic systems. They may also be used to treat hormonal dysfunction, cancer, atherosclerosis, wounds, tissue regeneration, hemophilia, leukemias, reperfusion injury, psoriasis and diabetes. Numerous examples of each type of disorder are given in the specification. Anti-GPCR-like protein antibodies are useful for detecting or quantitating the polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a food supplement.

Sequence      1314 AA;

Query Match	81.2%;	Score 1688.5;	DB 22;	Length 1314;
Best Local Similarity	82.4%;	Pred. No. 3.7e-15;		
Matches 327;	Conservative 24;	Mismatches 41;	Indels 5;	Gaps 2

QY 1 MSTSTLLATLAVLYVSGALVFOALFOPHEQQAOKMKDHGRQFLRDHPVCSQKSLD 60  
|||||  
540 MSTSTLLATLAVLYVSGALVFRALFQPHQDAQELGEVTEKFLIRHPVCSQDGL 509  
Db

[illegible]

121 CIPAAVAGIPFGMLTAGVDRGSSIRGIGHIEATPEKYNHVRGGLRSLASAVLFLIG 180  
 659 CIPAAVAGIPFGMLTAGVDRGSSIRGIGHIEATPEKYNHVRGGLRSLASAVLFLIG 180  
 181 CLFVLVLPPEVSESMESMLAEIAYIVYITLVYAGFGYGVGDGQNSPAIOPVFWMT 748  
 719 CILVLPPTFVFCYMEDWSKLEAIYIVATLVITLVYAGFGYGVGDGQNSPAIOPVFWMT 748  
 241 LFGIAVFAVALTITIGMWLRAVSRRTLRKEGGLTAAASVMTSTYMAVDTQSPGQVQVFWFI 708

SEQUENCE	RESULT
779 lldglayfaasviltitlignmllvavrtrraemgsltdgaaswltvtarvtlqraapaaappek	838
301 EOEPLPSSLEAPAVEPAGRGSPAPAEKVEETSPPTASLDYPSSENTAFIDEESDTOS	360
839 egpl-----lpppcpeagqlgrvtrpspspekakqpsptaaaldypsenaiaidessdtgs	894
361 ERGCALPAPRRRRRRNPNFSKPPSRPGRGRLRDKAVP	397
895 ergcplprapgrtrrrmpbrkpvtrlprgprdkgvp	931

ABB12229;  
11-JAN-2002 (first entry)  
Human K channel TRAAK homologue, SEQ ID NO:2599.  
Human; cytokine; cell proliferation

inhibin; chemotaxis; chemokinesis; tissue growth; immunomodulatory; activin; haematopoiesis regulation; tissue growth; immunomodulatory; growth factor; haematopoiesis regulation; tissue growth; immunomodulatory; growth factor; inhibin; chemotaxis; chemokinesis; tissue growth; immunomodulatory; activin; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; chronic inflammatory conditions; chronic inflammatory conditions; asthma; arthritis;

KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; vasotrophic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnereary; antitumor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-0503800.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX  
 PA (HXSE-) HXSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 DR WPI; 2001-457740/49.  
 DR N-PSDB; ABA09473.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 XX  
 PS Claim 20; Page 318; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoietic regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 421 AA;

Query Match 43.0%; Score 895; DB 22; Length 421;

Best Local Similarity 70.3%; Pred. No. 4.5e-68;  
 Matches 182; Conservative 18; Mismatches 19; Indels 40; Gaps 2;  
 QY 1 MNSTLLALLALVLYVSGALVLPQALRPHRQAKQKMDHRDQFLRBDHPVSGSKSLD 60  
 Db 163 MSTLLALLALVLYVSGALVLPQALRPHRQAKQKMDHRDQFLRBDHPVSGSKSLD 222  
 QY 61 FIKLVEALGGGANPETSMTSSNNHSSAMNLGSAFFSGTITTTI----- 105  
 Db 223 LKevada199gaadpetnstnsnsh-sawd1gsaffsgtlttt199gdwhv99gkelp 281  
 QY 106 -----GYGNIVLHTDAGRLFCIFVYALVGP1PFGMLAGVD 141  
 Db 282 hggcretegsqyaprlpasplcpygynvalrtadagrlfcifvaylplfg11la9yrd 341  
 QY 142 RLCSSLRKRGIGHEALFLKWHNPGLVRSLSANLFLICGLFVLPPTVFYSMSWSKL 201  
 Db 342 Rlgsslrhghleaaflwvhppe1vrsamlflllgcllflvlpctvfcymedwsk1 401  
 QY 202 EATYFVIVTLTVGFSDYV 220  
 Db 402 ealYfvivtlvtvgfdyv 420

# RESULT 7

ID AAY34133 standard; Protein; 411 AA.  
 XX AAY34133;  
 AC AAY34133;  
 DT 30-NOV-1999 (first entry)  
 XX  
 DE Human potassium channel K-Hnov59.  
 KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
 KW cardiovascular disorder; CNS disorder; renal disorder.  
 OS Homo sapiens.  
 XX  
 PN WO9943696-A1.  
 PD 02-SEP-1999.  
 XX  
 PF 22-FEB-1999; 99WO-US030826.  
 XX  
 PR 19-JAN-1999; 99US-0116448.  
 PR 25-FEB-1998; 98US-0076687.  
 PR 07-AUG-1998; 98US-0095836.  
 XX  
 PA (AAYS-) AAYS PHARM INC.  
 XX  
 PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;  
 DR WPI; 1999-527591/44.  
 DR N-PSDB; AA211915.  
 XX  
 PT New nucleic acids encoding mammalian K-Hnov potassium channel  
 PT proteins, useful for the diagnosis and treatment of episodic ataxia  
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome  
 XX  
 PS Claim 3; Page 104-105; 112pp; English.  
 XX  
 CC This sequence represents the human K-Hnov59 potassium channel.  
 CC K-Hnov proteins have a high degree of homology to known potassium  
 CC channels and may be alpha subunits, which form the functional channel,  
 CC or accessory subunits that act to modulate the channel activity. K-Hnov59  
 CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene  
 CC is located on chromosome 19, determined via PCR chromosomal  
 CC localisation using primers AA211939 and AA211940. K-Hnov cDNAs  
 CC were isolated by extension of expressed sequence tags (ESTs) which were  
 CC related but not identical to known human potassium channels. Potential  
 CC polymorphisms detected as sequence variants between multiple  
 CC independent clones. Potassium channels have critical roles in various



DR WPI: 2000-549146/50.  
 DR N-PSDB: AAD17496.  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties -  
 XX  
 PS Claim 3; Page 28; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anesthetic properties, producing a safe,  
 CC reversible state of unconsciousness with concurrent amnesia and analgesia  
 CC in a mammal upon inhalation. The present sequence is human TREK-1  
 CC potassium channel protein.  
 CC  
 XX  
 SQ Sequence 411 AA;  
 XX  
 Query Match 37.3%; Score 776.5; DB 21; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 5,7e-58;  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;  
 QY 1 MRSTLLALALVLYVSGALVFQALEOPHEQQAQKKMDHRDQFLRHPVYSOKSLSD 60  
 Db 42 mkwktvstiflvvlylligatvfkaleqphelsqrttlvlgkqtlfsgnscvnstelde 101  
 QY 61 FIKLVEALGGGANPETSMTNSSNHSSAMNLGSAFFESGTTITTYGNTVHTDAGRFL 120  
 Db 102 lqgivaalneglpr---lgnstnqishwdlgsffagvtlvtlfgnlsprteggkif 158  
 QY 121 CIEFALVGIPLFEGMLAGVDRGSSLRGIGITEAIFLKWHPGGLVRSLSAVPLILG 180  
 Db 159 cilyallgiprlfgllagvgdqlgtlfgkglakvedtlfkwnvsqtkiristliffilfg 218  
 QY 181 CLFVLPTPEFVSYSMSKLEAIFVITLTVGFGDVPDGTGQNSPAOPLWFWI 240  
 Db 219 cvltvalpaillfkhegwsaldalyfvltlctlgdgyaagsdleyldfkyprvwtwi 278  
 QY 241 LFGIAYFASVLTITGNMLRAVSRRTRAEMGGLTAQAASWTGTVTA 285  
 Db 279 lvglayfaavlsimgdwlrvlskktkeevgefrahnaeetantvta 323  
 XX  
 RESULT 10  
 AAB50044  
 ID AAB50044 standard; Protein; 411 AA.  
 XX  
 AC AAB50044;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human TREK.  
 XX  
 KW Human; TREK: 2P domain potassium channel; resting membrane potential;  
 KW neuronal excitability; neurotransmitter release modulation; epilepsy;  
 KW neurological disorder; sleep-related disorder; cognitive dysfunction;  
 KW attention deficit disorder; addiction; anxiety; phobia;  
 KW Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
 KW erectile dysfunction; alopecia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200072863-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 01-JUN-2000; 2000WO-GB02107.  
 XX  
 PR 01-JUN-1999; 99GB-0012733.  
 XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Hervieu GJ, Meadows HJ, Randall AD;  
 XX  
 DR WPI: 2001-080422/09.  
 DR N-PSDB: AAC90412.  
 XX  
 PT Use of human TREK1 polypeptide, polynucleotides encoding them and  
 PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
 PT disorders, addiction and dyskinesias including Parkinson's and  
 PT Huntington's chorea -  
 XX  
 PS Claim 7; Page 29; 35pp; English.  
 XX  
 CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
 CC 2P domain potassium channel family of proteins which play a part in the  
 CC control of resting membrane potential. Modulation of these channels will  
 CC therefore affect neuronal excitability, thereby leading to a modulation  
 CC of neurotransmitter release and activity of neuronal networks. Such  
 CC modulation therefore may be useful for the treatment of certain  
 CC neurological conditions such as epilepsy, sleep-related disorders,  
 CC cognitive dysfunction, attention deficit disorder, addiction,  
 CC anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
 CC incontinence, erectile dysfunction or alopecia.  
 CC  
 XX  
 SQ Sequence 411 AA;  
 XX  
 Query Match 37.3%; Score 776.5; DB 22; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 5,7e-58;  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;  
 QY 1 MRSTLLALALVLYVSGALVFQALEOPHEQQAQKKMDHRDQFLRHPVYSOKSLSD 60  
 Db 42 mkwktvstiflvvlylligatvfkaleqphelsqrttlvlgkqtlfsgnscvnstelde 101  
 QY 61 FIKLVEALGGGANPETSMTNSSNHSSAMNLGSAFFESGTTITTYGNTVHTDAGRFL 120  
 Db 102 lqgivaalneglpr---lgnstnqishwdlgsffagvtlvtlfgnlsprteggkif 158  
 QY 121 CIEFALVGIPLFEGMLAGVDRGSSLRGIGITEAIFLKWHPGGLVRSLSAVPLILG 180  
 Db 159 cilyallgiprlfgllagvgdqlgtlfgkglakvedtlfkwnvsqtkiristliffilfg 218  
 QY 181 CLFVLPTPEFVSYSMSKLEAIFVITLTVGFGDVPDGTGQNSPAOPLWFWI 240  
 Db 219 cvltvalpaillfkhegwsaldalyfvltlctlgdgyaagsdleyldfkyprvwtwi 278  
 QY 241 LFGIAYFASVLTITGNMLRAVSRRTRAEMGGLTAQAASWTGTVTA 285  
 Db 279 lvglayfaavlsimgdwlrvlskktkeevgefrahnaeetantvta 323  
 XX  
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 AAY30648  
 ID AAY30648 standard; Protein; 370 AA.  
 XX  
 AC AAY30648;  
 XX  
 DT 18-NOV-1999 (first entry)  
 XX  
 DE A mechanically sensitive potassium channel protein TREK-1.  
 XX  
 KW Mechanically sensitive potassium channel protein; TREK-1;  
 KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
 KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
 KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
 KW muscular disease.  
 XX  
 OS Mus sp.  
 XX  
 PN W09945108-A2.  
 XX









GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 4, 2002, 10:58:30 ; Search time 14.74 Seconds  
(without alignments)  
659,524 Million cell updates/sec

Title: US-09-655-272-2

Sequence: 1 MRSTTLALALVLYLVSG.....SKKPRPGGRLDKAPV 398

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUTS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/Dackfiltest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	776.5	37.3	411	US-09-236-080-2	Sequence 2, Appli
2	770.5	37.1	411	US-09-236-080-6	Sequence 6, Appli
3	761.5	36.6	370	US-09-144-914-8	Sequence 8, Appli
4	379.5	18.3	336	US-08-749-816-2	Sequence 2, Appli
5	379.5	18.3	336	US-09-144-914-2	Sequence 2, Appli
6	343	16.5	107	US-09-236-080-4	Sequence 4, Appli
7	332.5	15.7	405	US-09-144-914-5	Sequence 4, Appli
8	326.5	15.5	618	US-08-332-312-2	Sequence 4, Appli
9	301.5	14.5	336	US-08-332-312-4	Sequence 4, Appli
10	209	10.1	383	US-08-749-816-4	Sequence 7, Appli
11	198	9.5	383	US-09-144-914-7	Sequence 4, Appli
12	198	9.5	383	US-08-749-816-3	Sequence 6, Appli
13	184.5	8.9	347	US-09-144-914-6	Sequence 6, Appli
14	184.5	8.9	347	US-08-906-865-4	Sequence 6, Appli
15	132	6.3	696	US-08-956-242-13	Sequence 4, Appli
16	122	5.9	1593	US-08-628-829-4	Sequence 13, Appli
17	118	5.7	1159	US-08-956-242-13	Sequence 13, Appli
18	118	5.7	1159	US-09-351-215-13	Sequence 2, Appli
19	118	5.7	1159	US-09-226-012-2	Sequence 4, Appli
20	118	5.7	1159	US-09-226-012-2	Sequence 4, Appli
21	117	5.6	1083	US-09-600-776-2	Sequence 2, Appli
22	113	5.4	2293	US-09-368-590-2	Sequence 114, App
23	111.5	5.4	570	US-09-135-020-114	Sequence 80, App
24	111.5	5.4	570	US-09-135-021-114	Sequence 110, App
25	111.5	5.4	581	US-09-135-021-80	Sequence 2, Appli
26	111.5	5.4	581	US-09-135-010A-116	Sequence 2, Appli
27	111.5	5.4	676	US-09-135-021-2	Sequence 2, Appli

28	111.5	5.4	676	US-09-135-020-2	Sequence 2, Appli
29	111.5	5.4	676	US-09-135-010A-2	Sequence 2, Appli
30	111.5	5.4	676	US-09-634-920-2	Sequence 2, Appli
31	110	5.3	450	US-08-194-338-5	Sequence 5, Appli
32	109.5	5.3	960	US-09-219-849-5	Sequence 5, Appli
33	108	5.2	1323	US-08-026-138E-4	Sequence 4, Appli
34	107	5.1	169	US-08-483-533-28	Sequence 28, Appli
35	107	5.1	169	US-09-283-471A-28	Sequence 41, Appli
36	107	5.1	355	US-08-483-533-41	Sequence 41, Appli
37	107	5.1	355	US-09-283-471A-41	Sequence 3, Appli
38	107	5.1	355	PCT-0591-06532-3	Sequence 160, App
39	107	5.1	450	US-08-444-734A-8	Sequence 66, Appli
40	106.5	5.1	641	US-08-961-083-160	Sequence 33, Appli
41	106.5	5.1	357	US-07-609-716-66	Sequence 66, Appli
42	106.5	5.1	357	US-08-642-255-33	Sequence 66, Appli
43	106.5	5.1	357	US-08-475-411A-66	Sequence 66, Appli
44	106.5	5.1	357	US-08-478-029A-66	Sequence 6, Appli
45	105	5.1	297	US-08-580-545B-6	Sequence 6, Appli

#### ALIGNMENTS

RESULT 1  
US-09-236-080-2  
Sequence 2, Application US/09236080  
Patent No. 6242217  
GENERAL INFORMATION:  
APPLICANT: helen Meadows  
APPLICANT: Conrad Chapman  
TITLE OF INVENTION: No. 6242217el Compounds  
FILE REFERENCE: GP30031  
CURRENT APPLICATION NUMBER: US/09/236, 080  
CURRENT FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match 37.3%; Score 776.5; DB 4; Length 411;  
Best Local Similarity 49.8%; Pred. No. 2.4e-57;  
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;  
QY 1 MRSTTLALALVLYLVSGALVFOALQPHQQAQKMDHGRDPLRDPVCSQKSLD 60  
DB 42 MKMTVSTIFLVVLYLIGATVFKALQPHQPHISQRTTIVIOKOTFIQSHCVNSTELDE 101  
QY 61 FIKLLVAGLGANPESMTNSNHSAMNLSAEFFSGTITTTGYNIVLHNDARLF 120  
DB 102 LIOQIVAINNGITP---LQNTISQISHMDLSSFFFACTVTTTGFQNSIPRFGKIF 158  
QY 121 CIFALVGIPIFGMLLAGVCDRLGSSLRKIGIIEILFKMVPGLVRSJSAVFLDIG 180  
DB 159 CIYVALGIPFGFLLAGVGDOLGTFKGIKAVEDTFLKMNVSQTKIRIISTIFILFG 218  
QY 181 CLFVLTPTTFVFSFMSKLEAFVIVLTGFGDGVYPGDGCGNSPAQPIVPMFI 240  
DB 219 CILFVLTPTTFVFSFMSKLEAFVIVLTGFGDGVYPGDGCGNSPAQPIVPMFI 278  
QY 241 LFGVAFASVLTITGNMLRAVSRTKRAEMGTLNQAASWTGYTA 285  
DB 279 LVGLAVFAVLSMIDMLRVISKTKREVGFRHAHAEMTANYTA 323  
RESULT 2  
US-09-236-080-6  
Sequence 6, Application US/09236080  
Patent No. 6242217  
GENERAL INFORMATION:

APPLICANT: Helen Meadows  
 TITLE OF INVENTION: Conrad Chapman  
 FILE REFERENCE: GP30031  
 CURRENT APPLICATION NUMBER: US/09/236,080  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 6  
 LENGTH: 411  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-236-080-6

Query Match  
 Best Local Similarity 37.1%; Score 770.5; DB 4; Length 411;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

OY 1 MRSTLLALALVLYVSGALVFOALPOHEQOAKMDHGRDQFLRHPVCSOKSLSD 60  
 DB 42 MKMKVSTIFLVVLYLIGAVFKALEPOEISORTTIVIOKOTFLAOHACVNSTELDE 101  
 OY 61 FIKLVEALGGANPETSWTSSNHSAMNLSAFFFSGTITIGYGNVLTADGRLE 120  
 DB 102 LIQOIVAAINAGIIP---LGSSNOVSHMDLGSSFFAGVITITIGGNISPRTEGKTF 158  
 OY 121 CIFVALGIPLEGMLAGVDRIGSSLRGIGHEAIFLKMVPPGLVRSLSAVLELLIG 180  
 DB 159 CIYALLGIPLEGFLAGVGDQGTIFGKIAKVEDTFIKMNVSTKIRIISTIFILFG 218  
 OY 181 CILFVLTPFTFVSMSKLEAIFYVLTGVGFDVPGDGTGNSPAOPLVWFWI 240  
 DB 219 CVLFAVLPVIFKHEGMSALDAIFYEVITLTIGFDVAGSDIEYLDYFKPVWFWI 278  
 OY 241 LFGIAFASVLTITGNMLRAVSRRTAEKGLTQAASVTGVTA 285  
 DB 279 LVGLAYFAVLSMIGDWLRVSKTKKEVEGERAAHAEMTANVTA 323

RESULT 3  
 US-09-144-914-8  
 Sequence 8, Application US/09144914  
 Patent No. 6309855  
 GENERAL INFORMATION:  
 APPLICANT: Duprat, Fabrice  
 APPLICANT: Lesage, Florian  
 APPLICANT: Pink, Michel  
 APPLICANT: Lazdunski, Michel  
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 FILE REFERENCE: 989,6705CIP  
 CURRENT APPLICATION NUMBER: US/09/144,914  
 EARLIER FILING DATE: 1998-09-01  
 EARLIER APPLICATION NUMBER: 08/749,816  
 EARLIER FILING DATE: 1996-11-15  
 EARLIER APPLICATION NUMBER: 60/095,234  
 EARLIER FILING DATE: 1998-08-04  
 EARLIER APPLICATION NUMBER: FR 96/01565  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 8  
 LENGTH: 370  
 TYPE: PRT  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: TREK-1  
 US-09-144-914-8

Query Match  
 Best Local Similarity 36.6%; Score 761.5; DB 4; Length 370;  
 Pred. No. 3.8e-56;

Matches 141; Conservative 56; Mismatches 85; Indels 3; Gaps 1;  
 OY 1 MRSTLLALALVLYVSGALVFOALPOHEQOAKMDHGRDQFLRHPVCSOKSLSD 60  
 DB 42 MKMKVSTIFLVVLYLIGAVFKALEPOEISORTTIVIOKOTFLAOHACVNSTELDE 101  
 OY 61 FIKLVEALGGANPETSWTSSNHSAMNLSAFFFSGTITIGYGNVLTADGRLE 120  
 DB 102 LIQOIVAAINAGIIP---LGSSNOVSHMDLGSSFFAGVITITIGGNISPRTEGKTF 158  
 OY 121 CIFVALGIPLEGMLAGVDRIGSSLRGIGHEAIFLKMVPPGLVRSLSAVLELLIG 180  
 DB 159 CIYALLGIPLEGFLAGVGDQGTIFGKIAKVEDTFIKMNVSTKIRIISTIFILFG 218  
 OY 181 CILFVLTPFTFVSMSKLEAIFYVLTGVGFDVPGDGTGNSPAOPLVWFWI 240  
 DB 219 CVLFAVLPVIFKHEGMSALDAIFYEVITLTIGFDVAGSDIEYLDYFKPVWFWI 278  
 OY 241 LFGIAFASVLTITGNMLRAVSRRTAEKGLTQAASVTGVTA 285  
 DB 279 LVGLAYFAVLSMIGDWLRVSKTKKEVEGERAAHAEMTANVTA 323

RESULT 4  
 US-08-749-816-2  
 Sequence 2, Application US/08749816  
 Patent No. 6013470  
 GENERAL INFORMATION:  
 APPLICANT: Lesage, Florian  
 APPLICANT: Guillemae, Eric  
 APPLICANT: Pink, Michel  
 APPLICANT: Duprat, Fabrice  
 APPLICANT: Lazdunski, Michel  
 APPLICANT: Romey, Georges  
 APPLICANT: Barhanin, Jacques  
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
 TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WEISER & ASSOCIATES  
 STREET: 230 South Fifteenth Street, Suite 500  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/749,816  
 FILING DATE: 15-NOV-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weiser, Gerard J.  
 REGISTRATION NUMBER: 19,763  
 REFERENCE/DOCKET NUMBER: 989,6351P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-875-8394  
 TELEFAX: 215-875-8394  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 336 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-749-816-2

Query Match  
 Best Local Similarity 18.3%; Score 379.5; DB 3; Length 336;  
 Pred. No. 3.4e-24;

Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

OY 2 RSTLLALLAL-VLLYVSGALVQALQEPHEDQAKKMDHGRDQFLRHPQCSQKSLD 60  
 DB 18 RSAMCFGLVGLYLLVFGAVFSSVELPEYEDLLRQELKRRLEHEECLSEQOLQ 77

OY 61 FIKLLVLEALGGG---ANPETSWTSSNHNSSANNLGSAPFSGTITTTIGYCNIVLHTDA 116  
 DB 78 FLGRVLEASNNGSVLSNAGNNM-----WDFTSALFFASTVLTSTGYGHTVPLSDG 129

OY 117 GRLECFIYALVIGPLFGMLLAGVDRGSSL-RGIGHIAIFLKMHPGGLVRSLSAVL 175  
 DB 130 GKAFCTIISVIGIPFTLLFLTAVQRTVHTRRPVLFFH---IRMGFSKQVAIVHAVAL 186

OY 176 --FLILGCLLVLPFTFVSFVME-SWSKLEAIVFVITLTVGFGDVPDGTGON-SPA 231  
 DB 187 LGEVTVSCFFET--PAAVSVLEDDWNLDESFTCFISLSTIGLDGVVPEQGNQKREL 244

OY 232 YQPLVFWILFGLAFVASFVLT 253  
 DB 245 YKIGITCYLLGLLAMLVLET 266

RESULT 5  
 US-09-144-914-2  
 ; Sequence 2, Application US/09144914  
 ; Patent No. 6309855  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; FILE REFERENCE: 989,6705CIP  
 ; CURRENT APPLICATION NUMBER: US/09/144,914  
 ; EARLIER FILING DATE: 1998-09-01  
 ; EARLIER APPLICATION NUMBER: 08/749,816  
 ; EARLIER FILING DATE: 1996-11-15  
 ; EARLIER APPLICATION NUMBER: 60/095,234  
 ; EARLIER FILING DATE: 1998-08-04  
 ; EARLIER APPLICATION NUMBER: FR 96/01565  
 ; EARLIER FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 336  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: TWIK-1  
 ; US-09-144-914-2

Query Match 18.3%; Score 379.5; DB 4; Length 336;  
 Best Local Similarity 34.4%; Pred. No. 3,4e-24;  
 Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

OY 2 RSTLLALLAL-VLLYVSGALVQALQEPHEDQAKKMDHGRDQFLRHPQCSQKSLD 60  
 DB 18 RSAMCFGLVGLYLLVFGAVFSSVELPEYEDLLRQELKRRLEHEECLSEQOLQ 77

OY 61 FIKLLVLEALGGG---ANPETSWTSSNHNSSANNLGSAPFSGTITTTIGYCNIVLHTDA 116  
 DB 78 FLGRVLEASNNGSVLSNAGNNM-----WDFTSALFFASTVLTSTGYGHTVPLSDG 129

OY 117 GRLECFIYALVIGPLFGMLLAGVDRGSSL-RGIGHIAIFLKMHPGGLVRSLSAVL 175  
 DB 130 GKAFCTIISVIGIPFTLLFLTAVQRTVHTRRPVLFFH---IRMGFSKQVAIVHAVAL 186

OY 176 --FLILGCLLVLPFTFVSFVME-SWSKLEAIVFVITLTVGFGDVPDGTGON-SPA 231  
 DB 187 LGEVTVSCFFET--PAAVSVLEDDWNLDESFTCFISLSTIGLDGVVPEQGNQKREL 244

OY 232 YQPLVFWILFGLAFVASFVLT 253  
 DB 245 YKIGITCYLLGLLAMLVLET 266

RESULT 6  
 US-09-236-080-4  
 ; Sequence 4, Application US/09236080  
 ; Patent No. 6242217  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Helen Meadows  
 ; APPLICANT: Conrad Chapman  
 ; TITLE OF INVENTION: No. 6242217el Compounds  
 ; FILE REFERENCE: GP30031  
 ; CURRENT APPLICATION NUMBER: US/09/236,080  
 ; CURRENT FILING DATE: 1999-01-25  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-236-080-4

Query Match 16.5%; Score 343; DB 4; Length 107;  
 Best Local Similarity 58.1%; Pred. No. 8,7e-22;  
 Matches 61; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

OY 81 NSSNHNSSANNLGSAPFSGTITTTIGYCNIVLHTDAGLRFCTFYALVIGPLFGMLLAGV 140  
 DB 1 NSSNHNSSANNLGSAPFSGTITTTIGYCNIVLHTDAGLRFCTFYALVIGPLFGMLLAGV 60

OY 141 DRGSSLRGIGHIAIFLKMHPGGLVRSLSAVLFLICGLV 185  
 DB 61 DQGLTFGKIAKVEDTFIKMNSQTKRIITITIFILFGCLV 105

RESULT 7  
 US-09-144-914-5  
 ; Sequence 5, Application US/09144914  
 ; Patent No. 6309855  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; FILE REFERENCE: 989,6705CIP  
 ; CURRENT APPLICATION NUMBER: US/09/144,914  
 ; CURRENT FILING DATE: 1998-09-01  
 ; EARLIER APPLICATION NUMBER: 08/749,816  
 ; EARLIER FILING DATE: 1996-11-15  
 ; EARLIER APPLICATION NUMBER: 60/095,234  
 ; EARLIER FILING DATE: 1998-08-04  
 ; EARLIER APPLICATION NUMBER: FR 96/01565  
 ; EARLIER FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 405  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 ; FEATURE:  
 ; OTHER INFORMATION: TASK  
 ; US-09-144-914-5

Query Match 16.0%; Score 332.5; DB 4; Length 405;  
 Best Local Similarity 31.6%; Pred. No. 3,8e-20;  
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

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0Y 7 LALLALVLLVYSALVQALLQEPHEDQAKKDHRODFLEPDHCVSOKSLIEDFIKLLV 66
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Db 6 LALIVCFITVILVAAVFDALBESPEIEKRIET--RQLELARYNLBEGGELETERVYL 64
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 67 EALGGAGNETSWTNSSNHHSSAMNLGSAFFESGTTITTGIGNIYLPHDAGELCIFAL 126
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Db 65 RLKPHKAGVQ-----WRFGSEFYAIVTITIGYCHAMPSTDGGKVCYCMRYAL 112
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0Y 127 VGILFQMLLAGVDRGLSR-----RGIG--HIEAIFLKWHPGLYRSIAVLF 177
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 113 LGIFILIMQSLGERINTVRLILHRAKRGIGMRAIE-----VSMANVLLIG 160
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 178 LIGLLVLLPTEVFSYMESKLEAIVYVLTITVFGGDV--PCDGTGONSPAYQPL 235
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 161 FVSCISFLICGAAGAFSYEKWTFEPQAYYCFITLTITIGGDYVALQKQALQTPQY--- 217
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 236 VWEIILFGIAVFSVLTITGNMLRAVSR 264
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 218 ---VAFSFIILGLTVIGAFNLVYLR 242
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RESULT      8
US-09-144-914-4
: Sequence 4, Application US/09144914
: Patent No. 6309855
: GENERAL INFORMATION:
: APPLICANT: Duprat, Fabrice
: APPLICANT: Lesage, Florian
: APPLICANT: Fink, Michel
: APPLICANT: Lazdunski, Michel
: TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
: TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
: FILE REFERENCE: 989.6705C1P
: CURRENT APPLICATION NUMBER: US/09/144,914
: CURRENT FILING DATE: 1998-09-01
: EARLIER APPLICATION NUMBER: 08/749,816
: EARLIER FILING DATE: 1996-11-15
: EARLIER APPLICATION NUMBER: 60/095,234
: EARLIER FILING DATE: 1998-08-04
: EARLIER APPLICATION NUMBER: FR 96/01565
: EARLIER FILING DATE: 1996-02-08
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 394
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: TASK
US-09-144-914-4

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Query Match Similarity	15.7%	Score 326.5	DB 4	Length 394
Best Local Similarity	31.5%	Pred. No. 12e-19		
Matches	85	Conservative	45	Mismatches 95; Indels 45; Gaps 7

QY	7	LALLALVLLVSGALVEQALQPHNQQAQRKMDHGRDQFLDHPVCSQSKLEDFIKILV	66
Db	9	LALICFTFYLLVGAAYFADALESEPELLERQLEL-ROQELNARYNLSSGGVBEELERVYL	67
QY	67	EALGGANDETSMTSSNNHSAWNGSAFFESGTTITTTGYNIVLHTDAGLFCITFVAL	126
Db	68	RLPKHKAQVQ-----WRPAGSYFALITYITTTIGYHAAPSTDGGVFCMFVAL	115
QY	127	VGIPLEGMILLAGVGRGLSSLR-----RGIGHTEALFLKWHVPDGLVRSLSAVLELLI	179
Db	116	LGIPITLVMFOSLGRITVLYVLLHRAKKGIGMRA-----DVSMMNVLI	162
QY	180	G--CLLFVLTPTTFEYSMEYSWKSLEALFYVLTTLTGFGGDY--PGDGTQONSAPAQP	234
Db	163	GFESCISTLCIGAAAFSHYEHWTFPGQAVYYCFITLTITGFDGYVALQDQALQDTQY--	220

```

QY      235  LVMEMILFGLAYEASVLTITGNWLRASRR 264
          : | | : | | | : | |
Db      221  -----VAFSEVYILTLGLTIGAFNLNVYLR 245

```

```

1      RESULT 9
2      US-08-332-312-2
3      ; Sequence 2, Application US/08332312
4      ; Patent No. 5559026
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Price, Laura A.
9      ; APPLICANT: Pausch, Mark H.
10     ; TITLE OF INVENTION: Functional Expression of a Drosophila
11     ; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
12     ; NUMBER OF SEQUENCES: 4
13     ; CORRESPONDENCE ADDRESS:
14     ;
15     ; ADDRESSEE: American Cyanamid Company
16     ; STREET: One Cyanamid Plaza
17     ; CITY: Wayne
18     ; STATE: New Jersey
19     ; COUNTRY: US
20     ; ZIP: 07470-8426
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
27     ;
28     ; CURRENT APPLICATION DATA:
29     ; APPLICATION NUMBER: US/08/332,312
30     ; FILING DATE:
31     ;
32     ; CLASSIFICATION: 435
33     ; ATTORNEY/AGENT INFORMATION:
34     ; NAME: Harrington, James J.
35     ; REGISTRATION NUMBER: P-39,711
36     ; REFERENCE/DOCKET NUMBER: 32,421
37     ; TELECOMMUNICATION INFORMATION:
38     ; TELEPHONE: 201-831-3246
39     ; TELEFAX: 201-831-3305
40     ; INFORMATION FOR SEQ ID NO: 2:
41     ; SEQUENCE CHARACTERISTICS:
42     ; LENGTH: 618 amino acids
43     ; TYPE: amino acid
44     ; TOPOLOGY: linear
45     ;
46     ; MOLECULE TYPE: protein
47     ;
48     ; US-08-332-312-2

```

	Query Match	14.5%	Score 301.5:	DB 1:	Length 618;
	Best Local Similarity	27.7%;	Pred. No. 2,6e-17;		
	Matches	91;	Conservative	51;	Mismatches 111; Indels 75; Gaps 10;
OY	7 LALLALVLLIVSGALVFQALBQPHROQAQRKMDHDDOFLDHPHCVSQSKLEDFKLILY	66			
Db	: : : : : : : :	:	:	:	:
	7 ILLIFYIISYLMEGAIIYYHE-----HOEEKISRAEQKOAIANEY---LL	51			
OY	67 EALGG-----ANPSTNTSNNSHAMNLGSAFFPSGTITTTIGYNI	110			
	: : : : : : :	:	:	:	:
Db	52 ELGLDKNTTTTODELIQRISDYCDKRPVTLPPTDYDPYTTFEYHAFFAFVCSTGYGNI	111			
	: : : : : : :	:	:	:	:
OY	111 VLAHDAGRLFCFEVALVGIFLPGMILLAGDRISSLRIGHIEAIFPKW-----	161			
	: : : : : : :	:	:	:	:
Db	112 SPTTAGRMIMAIASVIIGIPVNGILFAGIGEYFGRT-----FAIIRRRKKRYKMSTD	164			
	: : : : : : :	:	:	:	:
OY	169 -HVPPGVLYRSLSAVLFLLIGCLLEVLTPTF-VESYMESMKLEAIYFIIVTLTVGFSDY	219			
	: : : : : : :	:	:	:	:
Db	165 HVPPEQLGITTTITALPGIALEFLVLCPOVGHILRELIGLISISLYSYVTTTIGFDY	224			
	: : : : : : :	:	:	:	:
OY	220 VPGDSTGONSP-----AYOPLVWEWILFGLAYFASVLTJTGNNLRARSRKTAEMLGT	273			
	: : : : : : :	:	:	:	:
Db	225 VPTFGANCPKEGCGFVVYQILEFYVWFLEFSIGYLMVMITFTTRGLDS-----RKLAYLE	278			
	: : : : : : :	:	:	:	:
OY	274 AQAAS-----WTGTVAIVATQTORTG	292			
	: : : : : : :	:	:	:	:

Db 279 QOLSSNLKATONRIMSG-----YTKDVG 301

# RESULT 10

US-08-332-312-4  
Sequence 4, Application US/08332312  
Patent No. 5559026

## GENERAL INFORMATION:

APPLICANT: Price, Laura A.  
APPLICANT: Pausch, Mark H.  
TITLE OF INVENTION: Functional Expression of a Drosophila  
TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332.312  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: P-831,711  
REFERENCE/DOCKET NUMBER: 32,4421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-332-312-4

Query Match 10.1%; Score 209; DB 1; Length 336;  
Best Local Similarity 29.3%; Pred. No. 6.5e-10;  
Matches 56; Conservative 32; Mismatches 53; Indels 50; Gaps 6;

QY 86 SSAMNLSGAFPSGTTITIGYGNIVLHTDAGRLFCIFALVGIPLFGMLAGVCDRL-- 143  
DB 25 TETWTFSSIFRAVYVVTITIGNPPVPTNIGRIMCILESLGIPLTIVTADLAGKFLS 84  
QY 144 -----GSSLR-----RGIGHIAIFLKWHPGVLRSLSA 173  
DB 85 EHLWLYGNYLKLKYLILSRHRRERHVCCHSHGMCHDMNIEEK-RIPAFVLAALI 143  
QY 174 VFLLIGCLFLVTPFVSYSMSKLAIFYVITLTVTGQGVDP-GDGTGONSPLY 232  
DB 144 VYTAFGVILM-----SKLEPMSFTSYWSFTMTVTGSGDLMRRDG-----Y 187  
QY 233 QPLVWFILFG 243  
DB 188 MYIILYIILG 198

# RESULT 11

US-08-749-816-4  
Sequence 4, Application US/08749816  
Patent No. 6013470

GENERAL INFORMATION:  
APPLICANT: Lesage, Florian  
APPLICANT: Guillemaire, Eric

APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunski, Michel  
APPLICANT: Roney, Georges  
APPLICANT: Barhanin, Jacques

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749.816  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 989.6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-749-816-4

Query Match 9.5%; Score 198; DB 3; Length 383;  
Best Local Similarity 26.7%; Pred. No. 6.5e-09;  
Matches 60; Conservative 42; Mismatches 95; Indels 28; Gaps 6;

QY 9 LLALVILYVSGALVFOALRQPH-----QOKKMDHGRDQFLRDHC---VSQKSLDEF 61  
DB 44 LVLSCTVYALGVALFLSLIEHPDELKRREKAIREFODLKQOFMGNITSGIENSQSIET 103  
QY 62 IKLVEALGGANP---ETSWTSSNHSAMNLSGAFPSGTTITIGYGNIVLHTDAGR 118  
DB 104 TKLILMEDNANMAEFYFLLPKDMVTFSSALVFTTVIIPVGYIFVVSAYGR 163  
QY 119 LFCITYALVGPRLGMLLAGYDRLGSSLRKIGIHIAIFLKWHPGVLRSLSAVFL 178  
DB 164 MCLINAVALLIGPLTLVYADTGKFAAQLVTRWFGDNN-----MAIPALIV- 209  
QY 179 IGCILFV--LPTFVSYSMSKLAIFYVITLTVTGQGVDP 221  
DB 210 --CLLFAIPLVVGFILCTSNITLYDSVYFSLTSTIFTIGFDLP 252

# RESULT 12

US-09-144-914-7  
Sequence 7, Application US/09144914  
Patent No. 6309855

## GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Fink, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING

RESULT 13  
 US-08-749-816-3  
 ; Sequence 3, Application US/08749816  
 ; Patent No. 6013470  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Guillemaire, Eric  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lazdunski, Michel  
 ; APPLICANT: Romey, Georges  
 ; APPLICANT: Barhanin, Jacques  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
 ; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
 ; TITLE OF INVENTION: OF DRUGS  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: WEISER & ASSOCIATES  
 ; STREET: 230 South Fifteenth Street, Suite 500  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/749,816  
 ; FILING DATE: 15-NOV-1996

```

; RESULT 14
; US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Flak, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.67050CP
; CURRENT APPLICATION NUMBER: US/09/144,914
; EARLIER FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
; US-09-144-914-6

```

Query Match 8.9%; Score 184.5; DB 4; Length 347;  
Best Local Similarity 25.8%; Pred. No. 7.7e-08;  
Matches 69; Conservative 41; Mismatches 74; Indels 83; Gaps 11;

QY 6 LLAALLAVLVLSGALVFALEQPHBOQAKMDHGRDQFLRDHPVCSOKSLEDFTIKL 65  
DB LSAITLVLFVNL-GAGIFLAETQNSSES-----LNNSSEVS-KCLHNL----- 82  
QY 66 VEALGGANPETS-----WTSSNHSANMLGSAFFSGTITITIGINIVLHTDAGRL 119  
DB 83 --PGGKTTAEMKSKLKCKLTKSSRID--GFGKAIFSWTLVSTVGSLYHSTLGRY 137  
QY 120 FCIFYATVGPPL-----FCMLLAG-----VGDRLGSSLR-----GI 151  
DB 138 LTIFFSLMTIPVFIATFEFGTFLAHLVYVSNRTLAIVKAYKLSQNPENATPSNLS 197  
QY 152 GHIAITFLKMHVPGLVRSLSAVLELLIGCLLVLTPTFVFSYMSKLEAIVFVITL 211  
DB 198 QHDYLIPLS-----SLLCSISLSSALFSSITENISYLSVYFGITM 241  
QY 212 TTVGFGDVPDGTGQNSPAYQPLVWF 238  
DB 242 FLIGIDIVPTN-----LVWF 257

## RESULT 15

US-08-906-865-4

Sequence 4, Application US/08906865

Patent No. 6040168

GENERAL INFORMATION:

APPLICANT: Greengard, Paul

APPLICANT: Porton, Barbara

APPLICANT: Kao, Hung-Teh

TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,865

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: /desc = "Synapsin Ia"

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

Query Match 6.3%; Score 132; DB 3; Length 696;  
Best Local Similarity 28.8%; Pred. No. 0.0048;  
Matches 42; Conservative 16; Mismatches 42; Indels 46; Gaps 5;

QY 289 QRTGP---SAPPEKEQPL-----LPSLIPAPPAVVP----- 318  
DB 475 QROGPPLOQRPPPGQOHLSGLCPPAGSPLPQRLPSPTSAPOQPASQAAPPPTQGGROSR 534  
QY 319 --AGRGPAPAEKVEPTSPPTASALDYPSENLAFTDESSDTQSERGALPRA---PRG 372  
DB 535 PVAGGPGAPPAAPAPASPS-----QROAGPPQATQRTSVSGPAPAPKASGAPPGC 584  
QY 373 RRRPNPSKKRSPRGGRRLDKAVPV 398  
DB 585 QOROGPPQKPPGPPPTROASQAGPV 610

Search completed: June 4, 2002, 11:00:34  
Job time: 124 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:58:45 ; Search time 20.89 Seconds  
(without alignments)  
1830.711 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079  
Sequence: 1 MKSTLLALLLVLLVIVSG.....SKPSRPRGRLRDKAVPV 398

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR\_71.\*

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379.5	18.3	336	2	S65566 inward rectifier p
2	353	17.0	1001	2	T13807 potassium channel
3	323.5	15.6	330	2	TC7703 TASK-5 protein - h
4	322	15.5	329	2	T43509 probable potassium
5	314.5	15.1	336	2	T132347 outward rectifier
6	298.5	14.4	364	2	T43361 probable potassium
7	291.5	14.0	334	2	T19860 hypothetical prote
8	279	13.4	528	2	T21834 hypothetical prote
9	269.5	13.0	392	2	T45032 hypothetical prote
10	269	12.9	524	2	T23907 hypothetical prote
11	265	12.7	393	2	T25392 hypothetical prote
12	261.5	12.6	443	2	T21598 hypothetical prote
13	257.5	12.4	522	2	T24265 hypothetical prote
14	248.5	12.0	513	2	T28933 hypothetical prote
15	242.5	11.7	1910	2	H88124 protein T12C9.3 [i
16	242	11.6	643	2	T26616 hypothetical prote
17	240.5	11.6	325	2	T15584 potassium channel
18	240	11.5	461	2	T43394 potassium channel
19	239.5	11.5	452	2	T21118 hypothetical prote
20	236.5	11.4	427	2	T27681 hypothetical prote
21	232.5	11.2	307	2	H89074 protein twk-24 [im
22	231.5	11.1	539	2	T23700 hypothetical prote
23	230	11.1	1539	2	T30037 hypothetical prote
24	229	11.0	551	2	T16426 potassium channel
25	229	11.0	555	2	T43357 potassium channel
26	228	11.0	485	2	T24201 hypothetical prote
27	223	10.7	444	2	T26229 hypothetical prote
28	220	10.6	383	2	T23182 hypothetical prote
29	218.5	10.5	484	2	T43529 probable potassium

30	218.5	10.5	519	2	T16629 hypothetical prote
31	216.5	10.4	335	2	S44635 f22b7.7 protein -
32	213	10.2	475	2	T27725 hypothetical prote
33	211	10.1	769	2	T27550 hypothetical prote
34	210	10.1	631	2	T26232 hypothetical prote
35	205	9.9	544	2	T43364 potassium channel
36	205	9.9	576	2	T43363 potassium channel
37	204	9.8	550	2	T22557 hypothetical prote
38	202.5	9.7	1136	2	T26953 hypothetical prote
39	201	9.7	381	2	T43393 potassium channel
40	199	9.6	681	2	T19429 hypothetical prote
41	198	9.5	383	2	T23746 hypothetical prote
42	197.5	9.5	569	2	T43531 probable potassium
43	194	9.3	586	2	T21683 hypothetical prote
44	193.5	9.3	757	2	T24266 hypothetical prote
45	192	9.2	405	2	T21188 hypothetical prote

## ALIGNMENTS

RESULT 1  
S65566  
inward rectifier potassium channel TWIK-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S65566  
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanl  
EMBO J. 15, 1004-1011, 1996  
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove  
A:Reference number: S65566; PMID:96183184  
A:Accession: S65566  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-336 <LES>  
A:Cross-references: EMBL:U03632; NID:g1086490; PIDN:AAB01688.1; PID:g1086491

Query Match 18.3%; Score 379.5; DB 2; Length 336;  
Best local similarity 34.4%; Pred. No. 2.2e-17;  
Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

QY 2 RSTLLALLLVLLVIVSGALVFOALQEPHOAKKMDHGDPLRDHPVCSOKSLD 60  
DB 18 RSANCFEVLGVLYLVFGAVFVSVELPYEDLLKRLKRRLEHECSEQLDQ 77  
QY 61 FIKLIVLALGCG---ANPETSWTNSSNHNLSAFAFFSGTITTTIGYGVNVLHTDA 116  
DB 78 FLGVLEASNYGVSLNASGNNM-----MDFTSLFFASTVLSTGTGHTVPLSDG 129  
QY 117 GRFCIFRVALVGFPGMLAGVADRGLSSI-RRGIGHIAIFLKMVRPPGLVRSAYL 175  
DB 130 GKACCIIVSYIGIPFTLLFVAVQRTVHYTRPVLYFH---TRWGFSAQVAIYAVL 186  
QY 176 --FLICGLFVLPTPTFVSYSME-SWSKLEAIYVITLTVGFGDVPDGTGON-SPA 231  
DB 187 LGFVIVSCFFI--PAAVFVLEDDMNFLESFYCFISLTIGLDVVPDGVNQRREL 244  
QY 232 YQPLVEMWILFGLAFVAVSLTT 253  
DB 245 YKIGITCYLLGLTAMLVLET 266

RESULT 2  
T13807  
potassium channel protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
C:Accession: T13807  
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.  
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996  
A:Title: OKR1, a potassium-selective leak channel with two pore domains cloned from D  
A:Reference number: Z17770; PMID:9705152

62 IEDFHEQQAQKMDHGRDQLRDPHPCVSKSLEDFT

outward rectifier potassium channel homolog twk-23 - *Caenorhabditis elegans*



C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T21834

R:Lennard, N.  
submitted to the EMBL Data Library, October 1996

A:Reference number: Z19476  
A:Accession: T21834

A>Status: preliminary; translated from GR/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-528 <WII>

A:Cross-references: EMBL:Z81077; PIDN:CAB03071.1; GSPDB:GN00019; CESP:F36A2.4

A:Experimental source: clone F36A2

C:Genetics:  
A:Gene: CESP:F36A2.4  
A:Map position: 1  
A:Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1

Query Match 13.4%; Score 279; DB 2; Length 528;  
Best Local Similarity 23.0%; Pred.No.1e-10;  
Matches 107; Conservative 53; Mismatches 126; Indels 180; Gaps 16;

OY 9 LIALVLLIVYSALVPQALEDPH----- 31  
| : ||| : |||| | |  
Db 21 LIGSVLVLIIGAIVFOMLEGEHLDFNSDFNEKHHFGPKMVKFFETIFRMSKGANFK 80  
| : ||| : |||| | |  
OY 32 -----EQQAOKKMD-----HGRODFLDHPVCOSKLSEDFIKILVEALGGA 73  
| : ||| : |||| | |  
Db 81 SALKKDDHAAKITDQNAKDVIDYDKLMSVAKKRDRKY-----KNVEDLKSYKEDTVDVF 131  
| : ||| : |||| | |  
OY 74 NPETSMT-----NSSNHSSAMNLGSAFPFSCITITTYGCVIVLTTDAGRFLCIIFY 124  
| : ||| : |||| | |  
Db 132 NDYVTFVFAHRVAVRHGGYDEDSPTWDFAANSVFETTTLTSLISGYVAPSTFGRLFGVIY 191  
| : ||| : |||| | |  
OY 125 ALVGIPLDGMLLAGGDRGLS-----RRGHIEATFLK----- 160  
| : ||| : |||| | |  
Db 192 CLIGIPLLVLYANAKFISSETIFFLHYELMNKCLEMKKRKRGEEVADPLOPMFGSDENE 251  
| : ||| : |||| | |  
OY 161 -----WHVPGPIVSLSAVLEFLLI-GCLLFVLTPEFVSYESMSKLEAIFYVT 210  
| : ||| : |||| | |  
Db 252 EEILLRVRLVLRPP-----LTVFEFVVGCI-----AAMVVRYMETWTYYVESLFIIFS 301  
| : ||| : |||| | |  
OY 211 LTTFEGFDYVPEDDGGQNSPAQPLVMFWILFGLAFASVLT-----I 254  
| : ||| : |||| | |  
Db 302 ILTVGFGDIRPSPGN-----IWVTLAFVVGIVLITTMCMQDVVGRMYLKEIHYL 349  
| : ||| : |||| | |  
OY 255 GNMLR-----AVSRRTFAEMGGLTAQAASTGTFTA-----RVTOR 290  
| : ||| : |||| | |  
Db 350 GKRLKSSNPFTYLLRRAKARRRAAMAASLLAQIAK--GMIFAHKOYNELARKSKRKKREKR 407  
| : ||| : |||| | |  
OY 291 TGPSAAPPEKEO-PLIPSSLPAAPVAVEPA-----GRGPSAP 327  
| : ||| : |||| | |  
Db 408 RGSHTVLPNKEKFARLPDPDPDCGVTSAYSVALMAPPFSPDP 453  
| : ||| : |||| | |

RESULT 9  
T45032  
hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45032

R:Wilson, R.; Alinscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johnson, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.; Nature 368, 32-38, 1994

A:Authors: Shownkeen, R.; Sims, M.; Smalton, N.; Smith, A.; Smith, M.; Sonhammer, E.; Slock, L.; Wilkinson-Sproot, J.; Wohlman, P.

A>Title: 2.2 Mb of continuous nucleotide sequence from chromosome III of C. elegans.

A:Reference number: S43531; MUID:94150718

A:Accession: T45032

A>Status: Preliminary; translated from GR/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-392 <WII>

[illegible]

```

QY 165 -----PGLVRSLS----- 172
Db 224 PNNNNPTAATAASAGCGTGRKKOORDVSNAGTFDNISETINDOSSEGENNEGEDEEQ 283
QY 173 -----AVLEFLIGCLLEFLTPTEVESYMSKLEAIYFVITLTGFGDIV 220
Db 284 IQPDSNHEKRVSVLEFLIMLGAVAGAYIVRMWEMETFEFAFYCFVTYTTIGFDIV 343
QY 221 PGDGTGNSPAYOPLVFWFLFLAFASVLTIGN-WLRASRRKRA-----EMGGIT 273
Db 344 PA-----NDWMLPATLAYIVFGLITTCIDLVGSEYIRDIHFYGRSLGRQPMITIGKV 397
QY 274 AQAASWTGTATARTORTGSPAPPPEKOPPLPSSLP-----APPAVVEPAGRP 322
Db 398 VHLCEVGVY-AFLQKNVGLTA-----EQITKLSQLPEEYILDLCLINGQPOLDMWIGRP 451
QY 323 GSPAPA---EKVETPSPPTASALDYSENIAFTIDESDTOSERGCLAPR-APR 371
Db 452 YVPPDIYFKWIEHP-----RTLSFASDRVLOSMSIDLNTSR-CSTARTLTPR 499

RESULT 11
T25392
Hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25392
R:Lloyd, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: 220027
A:Accession: T25392
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <MIL>
A:Cross-references: EMBL:Z92813; PIDN:CA807286.1; GSPDB:GN00021; CESP:T28A8.1
A:Experimental source: clone T28A8
C:Genetics:
A:Gene: CESP:T28A8.1
A:Map position: 3
A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match 12.7%; Score 265; DB 2; Length 393;
Best Local Similarity 24.8%; Pred. No. 5.8e-10;
Matches 77; Conservative 50; Mismatches 93; Indels 90; Gaps 8;

QY 7 LALLAVILYVSGALVFOALFOP-----HEQQAQKKMDHGRDQFLRDHP 51
Db 15 VSLIVLVVYVVGAFLEFLYQLEOPNEVEVRANIERFNHKKROMIEHLEMRESIGQHV 74
QY 52 C--VSOKSLEDFFIKLVEALG-----GGANPETSWTSSNHNSSANNLSAPFSS 98
Db 75 VEDLAVKYVDNVTIRLFEAFDTHCIGAKHLRPGCEDEYDNTYM-----TALFFT 124
QY 99 GTITTTIGGNIVLHTDARLFCIFAYALGIPFLFGMLAGVCDRLGSSLR----- 149
Db 125 TLLTLTIGGNLPTVGRKSLCTIALFGVPLILTVADIKFISENIVQLYTYRKLR 184
QY 150 -----GIGHIEAIFLKMHWPPGLVRSLSAVLELLIGCLFVL 186
Db 185 EKSKQKQYVSSSKDKKNKEDNLMDHLE-----NYISIPFLILVALLSYI 231
QY 187 T-PTFEVSYSWSKLEAIYFVITLTGFGDIVPGDGTGNSPAYOPLVFWFLIGLA 245
Db 232 TFGAVVLSMWEKWDFFSGFYSEFTMTVTFGDIV-----LKREYILDLCTYITIGLS 285
QY 246 YFASVLTIG 255
Db 286 ITTMCIDLVG 295

RESULT 12

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T21598
Hypothetical protein F31D4.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21598
R:Mortimore, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: 219447
A:Accession: T21598
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-443 <MIL>
A:Cross-references: EMBL:Z92832; PIDN:CA807375.1; GSPDB:GN00023; CESP:F31D4.7
A:Experimental source: clone F31D4
C:Genetics:
A:Gene: CESP:F31D4.7
A:Map position: 5
A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 12.6%; Score 261.5; DB 2; Length 443;
Best Local Similarity 27.5%; Pred. No. 1.1e-09;
Matches 84; Conservative 49; Mismatches 96; Indels 77; Gaps 10;

QY 9 LLALVILYVSGALVFOALFOPHEQQAQ-----KKMDHGRDQFLRD 49
Db 17 LIIYFLIYICISGLVFWLIEEPYQSELRDAMQHKIENNRPAVDAMMKRIFNNSDYLIYI 76
QY 50 HPCVSOKSLEDFFIKLVEALGCGANP-ETSWTSSNHNSSANNLSAPFSGTITITIGV 108
Db 77 KGMTSQRLTFFFI-----ELGSEYENQGVKW---SOKKMDMNNNAVLPAGTICTTITIGV 129
QY 109 NIVLHTDAGRLFCIFAYALGIPFLFGMLAGVCDRLGSSLRGIGHIEAIFLKMHWPPGLV 168
Db 130 HLYPMTDGRKMTMIFALFGIPMLVLVQDQKGLITTMK-----FPWFQYRKRLM 179
QY 169 RSLSAV-----LFLIGCLVLPPTVFFSYM-----ESWS 199
Db 180 RRIIMCCTKQPIEEKKEIERQBRHDLDFDLPVGLAL-IYWIIFICSVLSVMDHNMV 238
QY 200 KIEAIYFVITLTGFGDIVPGDGTGNSPAYOPLVFWFLIGLAFFASVLTITGNMLR 259
Db 239 LLESFFFTSLSTVGLDLPV-----SSPRLITMGTFLVGL-----SLYSNVILIQ 288
QY 260 AVSRRT 265
Db 289 AKKKS 294

RESULT 13
T24265
Hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24265
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: 219866
A:Accession: T24265
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <MIL>
A:Cross-references: EMBL:Z70036; PIDN:CA93875.1; GSPDB:GN00028; CESP:T01B4.1
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CESP:T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.4%; Score 257.5; DB 2; Length 522;
Best Local Similarity 26.1%; Pred. No. 2.4e-09;
Matches 79; Conservative 42; Mismatches 87; Indels 95; Gaps 10;

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Query Match	46.6%	Score 969	DB 11	Length 186
Best local Similarity	98.4%	Pred. No. 2	Le-64	
Matches 182	Conservative 1	Mismatches 2	Indels 0	Gaps 0
QY	214	VGFEGDVPDGTGQNSPAPVQPLVWFMLEFGATYFASVLTITGNMLRAVSRRTRAEMGGLT	273	
Db	2	VGFEGDVPDGTGQNSPAPVQPLVWFMLEFGATYFASVLTITGNMLRAVSRRTRAEMGGLT	61	
QY	274	AAAAAWTGTGYARVYQRTGFSAAPPEKEQPLLPSSLPAPAVVEPACRPGSPAPAEKVE	333	
Db	62	AAAAAWTGTGYARVYQRTGFSAAPPEKEQPLLPSSLPAPAVVEPACRPGSPAPAEKVE	121	
QY	334	PSPFASALDYPSSENTLATIDESSPTQSRGCALPRAPGRGRRRPNPSKTPSRPFGRLD	393	
Db	122	PSPFASALDYPSSENTLATIDESSPTQSRGCALPRAPGRGRRRPNPTKPSRPGRLD	181	
QY	394	KAVPV 398		
Db	182	KAVPV 186		
RESULT	3			
Q9NRT2		PRELIMINARY	PRT	411 AA.
Q9NRT2				
Q9NRT2		01-OCT-2000 (TIREMBLrel. 15, Created)		
Q9NRT2		01-OCT-2000 (TIREMBLrel. 15, last sequence update)		
Q9NRT2		01-DEC-2001 (TIREMBLrel. 19, last annotation update)		
Q9NRT2		TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.		

[illegible]

	RESULT	4	
ID	092414		
AC	092414	PRELIMINARY;	PRT; 370 AA.
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DDT	01-DEC-2001	(TREMBLrel. 19, last sequence update)	
DR	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
OS	Mechanosensitive tandem pore potassium channel.		
OC	Rattus norvegicus (Rat).		
OX	Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
NCBI_MxId:	Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
NCBI_TaxID:	10116;		
[1]			
SEQUENCE FROM N.A.			
STRAIN=SPRAGUE-DAWLEY;			
MEDLINE=21268449; PubMed=11374070;			
Kim Y., Bang H., Gnatenco C., Kim D.;			
"Synergistic interaction and the role of C-terminus in the activation			
of TRAAK K <sup>+</sup> channels by pressure, free fatty acids and alkali.";			
Pfluegers Arch. 442:64-72(2001).			
EMBL; AF302842; AAK60504.1; -			
Ionic channel.			
KW			



RP SEQUENCE FROM N.A.  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL136087; CAC07336.1; -  
 DR InterPro: IPR003280; 2porek\_channel.  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 294 AA; 32507 MW; FCBA3B352F1F0952 CRC64;

Query Match 23.6%; Score 490; DB 4; Length 294;  
 Best Local Similarity 40.8%; Pred. No. 1,1e-28;  
 Matches 102; Conservative 54; Mismatches 78; Indels 16; Gaps 5;

DB 6 LIALALVLLVLYSGALVFOALFQALPHEQQAOKKMDGRDQFLRDHPVCSQKSLDEFTKL 65  
 14 VLPLLVAVCYLLGATFOLLERQAEQSRDQFQLEKLFLENITCLOMAEQFQVY 73  
 QY 66 VEALGGANPETSWTSSNSSAMNLSAFAFFSGTITTTGIGNIVLHTDAGRLFCIFYA 125  
 DB 74 MEAWKGVNPRGNSTNSN-----WDESSSFAGTAVTTIGYGNLAPSTEAGQVCEVYA 129  
 QY 126 LVGIPLEGMLLAGYGRDLGSSLRGIGHTEAIFLKWHPV---GIVRSLSAVLFLIGL 182  
 DB 130 LAGIPLVIFL---NHLGTGLRAHLAIE---RREDPRRSQVLYQVIGLALFTLTGL 181  
 QY 183 LFTVTFEVSMSKLEAIFVITLTGFGDYVPG-DGTGONSAPVQPLWFWIL 241  
 DB 182 VIIIFPMVTSHEGMSFSGEYFAFITLTSTIGFGDYVGTDPKSHYISVRSLSAIVIL 241  
 QY 242 FGIAVFAVSL 251  
 DB 242 LGLAWLALIL 251

RESULT 8  
 Q9BXDI PRELIMINARY; PRT; 343 AA.  
 AC Q9BXDI;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PORASSIUM CHANNEL TASK-4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ADRENAL GLAND;  
 RX MEDLINE=21145510; PubMed=11248242;  
 RA Decher N., Maier M., Dittlich W., Gassenhuber J., Bruggemann A.,  
 RA Busch A.E., Steinmeyer K.;  
 RT "Characterization of TASK-4, a novel member of the pH-sensitive, two-  
 RT pore domain potassium channel family.";  
 RL FEBS Lett. 492:84-89(2001).  
 DR EMBL: AF339912; AAK28551.1;  
 DR InterPro: IPR003280; 2porek\_channel.  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 SQ SEQUENCE 343 AA; 38172 MW; 29B1F354CE22E3BB CRC64;

Query Match 20.9%; Score 433.5; DB 4; Length 343;  
 Best Local Similarity 36.2%; Pred. No. 1.9e-24;  
 Matches 111; Conservative 49; Mismatches 120; Indels 27; Gaps 7;

DB 22 TVLLLA-VLAVIALGTGVFTLEGRAQDSSRSPQRKDWELLNFTCLDRPALDSLIRD 80  
 QY 65 LVEALGGANPETSWTSSNSSAMNLSAFAFFSGTITTTGIGNIVLHTDAGRLFCIFY 124  
 DB 81 VQAKRKNGA-----SLNSTSMGRWELVGSFFSVSTTTIGYGNLSPNTMAARLFCIFY 136  
 QY 125 ALVGPLEGMLLAGYGRDLGSSLRGIGHTEAIFLKWHPVPGVRSLSAVLFLIGCLIF 184  
 DB 137 ALVGIPLVLYL---NRLGHLMOQGVNHHASRLGCTWOPDPAKRWLAGSALLGLLIF 192  
 QY 185 VTFEVSMSKLEAIFVITLTGFGDYVPGDGTGONSAP-YQPLWFWILFG 243  
 DB 193 LILPLFLSHHEGMSYEGEYFAFITLTSTIGFGDYVGNMPSORPLWTKKNVSLMILFG 252  
 QY 244 LAYRASVLTITGNMLRAVSRT---RAEMGGLTAQASWTCVTVARVQR--TGPSADP 297  
 DB 253 MA-----WLAISNSSSPSMRROGGYPAATYTLRLRTSSPRAGDRDLTGOSQPT 301  
 QY 298 PEKQPL 304  
 DB 302 PHSKDAI 308

RESULT 9  
 Q96T54 PRELIMINARY; PRT; 332 AA.  
 AC Q96T54;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 2P DOMAIN POTASSIUM CHANNEL TASK-2.  
 GN CNK17.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,  
 RA Lazdunski M., Lesage F.;  
 RT "Genomic and functional characteristics of novel human pancreatic 2P  
 RT domain K<sup>+</sup> channels.";  
 RL Biochem. Biophys. Res. Commun. 0:0-0(2001).  
 DR EMBL: AF358910; AAK49533.1; -  
 KW Ionic channel.  
 SQ SEQUENCE 332 AA; 36894 MW; 1848DBC06E078158 CRC64;

Query Match 20.6%; Score 428.5; DB 4; Length 332;  
 Best Local Similarity 36.0%; Pred. No. 4.4e-24;  
 Matches 111; Conservative 49; Mismatches 115; Indels 33; Gaps 8;

QY 4 TTLALALVLLVLYSGALVFOALFQALPHEQQAOKKMDGRDQFLRDHPVCSQKSLDEFTK 63  
 DB 21 STVLLLA-VLAVIALGTGVFTLEGRAQDSSRSPQRKDWELLNFTCLDRPALDSLIR 79  
 QY 64 LVEALGGANPETSWTSSNSSAMNLSAFAFFSGTITTTGIGNIVLHTDAGRLFCIFY 123  
 DB 80 DVQAYKNGA-----SLNSTSMGRWELVGSFFSVSTTTIGYGNLSPNTMAARLFCIFY 135  
 QY 124 YALVGPLEGMLLAGYGRDLGSSLRGIGHTEAIFLKWHPVPGVRSLSAVLFLIGCLIF 183  
 DB 136 FALVGIPLVLYL---NRLGHLMOQGVNHHASRLGCTWOPDPAKRWLAGSALLGLLIF 191  
 QY 184 VTFEVSMSKLEAIFVITLTGFGDYVPGDGTGONSAP-YQPLWFWILF 242  
 DB 192 LILPLFLSHHEGMSYEGEYFAFITLTSTIGFGDYVGNMPSORPLWTKKNVSLMILF 251  
 QY 243 GLAVFAVLTITGNMLRAVSRT---RFAEMGGLTAQASWTCVTVARVQR--TGPSA 295  
 DB 252 GNAWALALITKLISOLETPGRVCSCHHSKEDP-----KSGSW-----RQGPDR 296

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OY 296 PPEKEOP 303
Db 297 -EPESHSP 303

RESULT 10
OYK62 PRELIMINARY; PRT; 502 AA.
ID OYK62:
AC OYK62:
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-OCT-2001 (TREMREL. 18, Last annotation update)
DE POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
GN KCKN5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=KIDNEY;
RA Roux J., Barhanin J.;
RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Cid L.P., Niemeyer M.I., Sepulveda F.V.;
RT "Functional properties of mouse TASK-2 potassium channel."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259395; AAF6868.1;
DR MGD; MGI:1336175; AAG35065.1;
DR KCKN5;
DR InterPro; IPR003280; 2porek_channel.
DR InterPro; IPR000636; Cation_chan_nov_119.
DR InterPro; IPR001622; Channel_pore_K.
DR Pfam; PF00520; ion_trans_1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR Ionic channel.
SQ SEQUENCE 502 AA; 55976 MW; EAC7EC71B44D95 CRC64;

Query Match 20.3%; Score 421; DB 11; Length 502;
Best Local Similarity 26.8%; Pred. No. 2.6e-23;
Matches 129; Conservative 70; Mismatches 147; Indels 136; Gaps 20;

OY 9 LALVLVLYSGALVFOALEOPHEQAOAKMDHGRDQFLRDHPCVSKSLEDFTKLVEA 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8 LTAIIFVLAIGALFEVLEPHEKAKNYTKLHLKEPPCLSQGLDKILQVSDA 67
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 69 LGGGANPETSNNSSNHSANMLGSAFFPSGITTTTIGGNVLTMDAGRLFCIFYALVG 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 ----ADGCAITGNQTFNN-WMPPNMTFPAATVITTTIGGNVAPKTPAGRLFCIFYALVG 122
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 129 IPL-----FGLLAGVGRGLSSSL-RRGIG-----HIEAIFLKMHPGGLVNSLSAV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VPLCLTWISALGKFGGGRKRLGQFLTRGVSLRKAQITCFATFIW-----169
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 175 LFLILGCLFVLPTFEVFSYMSKLEAIYVIYVLTGVDGYVPGDGTONSPA-YQ 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 ----GLVHLVLPFVFMVTEEMNYIEGLYSFITISTIGFGDFAGVNPSSANTHALYR 224
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 234 PLVWFVTLFGLAFASVLTITIGNL-----RAVSRRFR-----AEMG 270
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 YFVELMILYGLAW-----LSLEVMKYSMVEYHKAIKRRRRKRESFESSPRKALQMA 280
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 271 GLPA-----QASMTGTV-----TARVTOGTSPSAP-----PEKEQPLIP 306
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 GSTASKOVNIFFSLKKEERYNDLIQIKGKAMKTSGGGRVGPCHGLGPOGDRPLPTIP 340
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 307 SSLPAP-----PAVVE-----PAG-RQSGPARPAKVT-----333
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 341 ASL-APLVVYSKNRPVSLVEYSQTLKNKGHVSRLGEENGAQAPKDSYOTSEVFIMQDR 399
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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OY 334 --PSPPTASALDY-----PSENLAFFIDESDYSERGCALPRAPRRRRPPKSPRR 386
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 400 ISEGEPEWALDYHPLIFONANTIFENE-----ETGLSDEETSKSVSDNLTISKQEPQ 453
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 387 GP 388
Db 454 GP 455

RESULT 11
OYKX8 PRELIMINARY; PRT; 241 AA.
ID OYKX8:
AC OYKX8:
DT 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE 3010005K24RIK PROTEIN.
GN 3010005K24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Salto T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Salto K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norcone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK019376; BAB31686.1;
DR MGD; MGI:1924704; 3010005K24RIK.
DR InterPro; IPR001622; Channel_pore_K.
SQ SEQUENCE 241 AA; 25799 MW; B4C39F77CD0A39DA CRC64;

Query Match 20.0%; Score 415.5; DB 11; Length 241;
Best Local Similarity 46.1%; Pred. No. 2.8e-23;
Matches 88; Conservative 32; Mismatches 48; Indels 23; Gaps 4;

OY 1 MRSTLALALVLYSGALVFOALEOPHEQAOAKMDHGRDQFLRDHPCVSKSLED 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 MKKTVVAIVVVVVVLYVGLVGRALFQPFSSQKNTALTKAPFLDHICVSPQELT 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 61 FIKLVEALGGANPETSNNSSNHSANMLGSAFFPSGITTTTIGGNVLTMDAGRLFCIFYALVG 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 LIQHALLADADNAGVSPV-----GNSSNSSSHWDLSGAFFAGTAVITTTIGGNVAPKTPAGRLFCIFYALVG 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 121 CIFVALVGLPFLGCLAGVGRGLSSSLRKGIGHIEAIFLKMHPGGLVNSLSAVLFLILG 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 CILVAIFGIFLFGFLAGIDGGLTIFGKSIAVEVVF-RAH-----G 225
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 CLFLVLPTEV 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 C-FVCTHIFV 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 12  
Q9ERU5 PRELIMINARY; PRT; 313 AA.  
ID Q9ERU5  
RT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)  
DE 2P DOMAIN K+ CHANNEL, TWIK-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RC MEDLINE=20435832; PubMed=10887187;  
RA Patel A.J., Malingret F., Magnone V., Fosset M., Lazdunski M.,  
RA Honore E.,  
RT "TWIK-2, an inactivating 2P domain K+ channel.",  
RL J. Biol. Chem. 275:28722-28730(2000).  
DR EMBL; AF281304; AAG10508.1; -  
DR InterPro: IPR003280; 2porek\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR Pfam: PF00520; Ion\_trans\_1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01096; TWIK1CHANNEL.  
KW Ionic channel.  
SQ SEQUENCE 313 AA; 34214 MW; A93629568785CDBF CRC64;

Query Match 18.8%; Score 390; DB 11; Length 313;  
Best Local Similarity 35.1%; Pred. No. 2.9e-21;  
Matches 98; Conservative 50; Mismatches 101; Indels 30; Gaps 8;  
QY 8 ALLATVLT-----YLVSGALVFQALPQHPHQQAOKKMDGRQFLRDHCVCYSOKSLIEDFIK 63  
DB 5 ALLASALVAAYGYLGLALLVARLERPHEARLRARLGLRLQDLNHSQVAAHMLDAVE 64  
QY 64 LIVERA-----LGGANPETSMTNSSNHSANLGSAPFSGTITITIGYGNIVLHTDA 116  
DB 65 RYLAAGRLGRAVLNANASGP---ANASD--PAMDFASALFFASLIVTMGGYTTPLTDA 118  
QY 117 GLRLEIFALVGLPFGMLLAGVGRGLSSLRGIGITEAIFLKWHPVPGSLASVLF 176  
DB 119 GKASIVYALGVPTTMLLTLASAQRL--SLTLTHAPLSWLSLRGWHMPQPARAHMLVAL 176  
QY 177 LLIGCLFVLPTFEVFSYM-ESMSKLEAIVYVTLTTFVGFGDYVPGDGTGQ-NSPAYOP 234  
DB 177 LMVIAIFELIPAAVVFLEAWFELAFYCFISLSTIGLDYVPGDAPQYRSLKYV 236  
QY 235 LVMFMILFGLAYFASVLTITGNMLRANVSRTRAMGGIT 273  
DB 237 LVTAIFLGLVAVLVLOTF-----RVSDLHGLT 266

RESULT 13  
Q922T2 PRELIMINARY; PRT; 336 AA.  
AC Q922T2  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)  
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)  
DE PUTATIVE POTASSIUM CHANNEL, TWIK.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gen L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,

RA Kaczmarek L.K.;  
RT "Cloning and localization of rTWIK, a putative potassium channel with  
RT two P domains.",  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF022819; AAD09336.1; -  
DR InterPro: IPR003280; 2porek\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR Pfam: PF00520; Ion\_trans\_1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01096; TWIK1CHANNEL.  
KW Ionic channel.  
SQ SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 18.1%; Score 376.5; DB 11; Length 336;  
Best Local Similarity 34.4%; Pred. No. 3.2e-20;  
Matches 90; Conservative 53; Mismatches 96; Indels 23; Gaps 9;  
QY 2 RSTLLALLAL-VLLYVSGALVFQALPQHPHQQAOKKMDGRQFLRDHCVCYSOKSLIED 60  
DB 18 RSAMCFGLVLYGLLYLVFGAVFSSVELPYEDLLRQLKRLRRLHEHCLSEPOLBQ 77  
QY 61 FIKLLEALGGG---ANPETSMTNSSNHSANLGSAPFSGTITITIGYGNIVLHTDA 116  
DB 78 FLGRVLEASNTGVSLVSNASGNN-----WDFTSALFFASTVLTGCGHTVPLSDG 129  
QY 117 GLRLEIFALVGLPFGMLLAGVGRGLSSLRGIGITEAIFLKWHPVPGSLASVLF 175  
DB 130 GKAFCIIVSYIGIPFTLLFLTAVQRTVAVTRRPVLYEH---IRNGFSQVAYAIYHAYL 186  
QY 176 -FLIGCLFVLPTFEVFSYM-ESMSKLEAIVYVTLTTFVGFGDYVPGDGTGQ-SPA 231  
DB 187 LGFTVYSCFFPL-PAAVFSLIEDWNLFESFYCFISLSTIGLDYVPGEGYNOQFREL 244  
QY 232 YQPLVFWILFGLAYFASVLT 253  
DB 245 YKIGITCYLLGLLMLVLET 266

RESULT 14  
Q99L99 PRELIMINARY; PRT; 336 AA.  
AC Q99L99  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
DE POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1.  
GN KCKNK1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003729; AA03729.1; -  
DR MGD; MGI:109322; Kcnk1.  
DR InterPro: IPR003280; 2porek\_channel.  
DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR Pfam: PF00520; Ion\_trans\_1.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01096; TWIK1CHANNEL.  
SQ SEQUENCE 336 AA; 38201 MW; 76B7FD5361A6216C CRC64;

Query Match 18.1%; Score 376.5; DB 11; Length 336;  
Best Local Similarity 34.4%; Pred. No. 3.2e-20;  
Matches 90; Conservative 53; Mismatches 96; Indels 23; Gaps 9;

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